```
                    GenCore version 4.5
           Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on:   July 15, 2002, 11:04:30 ; Search time 13.05 Seconds
                                    (without alignments)
                                    591.455 Million cell updates/sec

Title:          US-09-671-658A-2
Perfect score:  316
Sequence:       1 MRRASRDYGKYLRSSEEMGS........LLDPDQDATYFGAFKVQDID 316

Scoring table:  OLIGO
                Gapop 60.0 , Gapext 60.0

Searched:       231628 seqs, 24425594 residues
d size :        0
Total number of hits satisfying chosen parameters:   231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 50 summaries

Database :   Issued_Patents_AA:*
         1:  /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
         2:  /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
         3:  /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
         4:  /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
         5:  /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
         6:  /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
```

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	316	100.0	316	2	US-08-842-842-7	Sequence 7, Appli
2	316	100.0	316	4	US-08-989-362-2	Sequence 2, Appli
3	316	100.0	316	4	US-09-052-521C-2	Sequence 2, Appli
4	217	68.7	294	3	US-08-996-139-11	Sequence 11, Appli
5	217	68.7	294	4	US-08-995-659-11	Sequence 11, Appli
6	217	68.7	294	4	US-09-215-649A-11	Sequence 11, Appli
7	27	8.5	28	4	US-09-052-521C-34	Sequence 34, Appli
8	22	7.0	27	4	US-09-052-521C-33	Sequence 33, Appli
9	22	7.0	317	3	US-08-996-139-13	Sequence 13, Appli
10	22	7.0	317	4	US-08-995-659-13	Sequence 13, Appli
11	22	7.0	317	4	US-09-215-649A-13	Sequence 13, Appli
12	22	7.0	317	4	US-09-052-521C-4	Sequence 4, Appli
13	17	5.4	17	4	US-09-052-521C-35	Sequence 35, Appli
14	8	2.5	459	2	US-08-870-518-2	Sequence 2, Appli
15	8	2.5	4472	2	US-08-804-227C-2	Sequence 2, Appli
16	7	2.2	21	4	US-08-997-080-4	Sequence 4, Appli
17	7	2.2	21	3	US-08-873-970-4	Sequence 4, Appli
18	7	2.2	21	4	US-09-095-855-4	Sequence 4, Appli
19	7	2.2	21	4	US-08-705-347A-4	Sequence 4, Appli
20	7	2.2	21	4	US-09-324-542-4	Sequence 4, Appli
21	7	2.2	41	2	US-08-640-847C-3	Sequence 3, Appli
22	7	2.2	41	2	US-08-640-847C-9	Sequence 9, Appli
23	7	2.2	41	2	US-08-640-847C-12	Sequence 12, Appli
24	7	2.2	58	2	US-08-284-391B-35	Sequence 35, Appli
25	7	2.2	58	2	US-09-218-950-35	Sequence 35, Appli
26	7	2.2	93	1	US-09-591-498-10	Sequence 10, Appli
28	7	2.2	93	1	US-08-591-498-14	Sequence 14, Appl
29	7	2.2	117	3	US-08-702-609A-4	Sequence 4, Appl
30	7	2.2	117	3	US-08-702-609A-6	Sequence 6, Appl
31	7	2.2	190	3	US-08-799-149C-3	Sequence 3, Appl
32	7	2.2	207	4	US-09-199-637A-211	Sequence 211, App
33	7	2.2	223	4	US-09-171-461-11	Sequence 11, Appl
34	7	2.2	301	1	US-08-420-235B-47	Sequence 47, Appl
35	7	2.2	301	2	US-08-343-101A-22	Sequence 22, Appl
36	7	2.2	301	2	US-09-183-688-22	Sequence 22, Appl
37	7	2.2	301	4	US-08-799-624-47	Sequence 47, Appl
38	7	2.2	337	2	US-08-861-464-12	Sequence 12, Appl
39	7	2.2	337	4	US-08-396-001-12	Sequence 12, Appl
40	7	2.2	337	4	US-09-323-433A-12	Sequence 12, Appl
41	7	2.2	370	4	US-09-142-551A-4	Sequence 4, Appl
42	7	2.2	375	3	US-08-872-979-3	Sequence 3, Appl
43	7	2.2	396	4	US-09-142-551A-3	Sequence 3, Appl
44	7	2.2	422	2	US-08-485-938A-34	Sequence 34, Appl
45	7	2.2	468	2	US-08-390-000A-7	Sequence 7, Appl
46	7	2.2	472	1	US-08-194-338-6	Sequence 6, Appl
47	7	2.2	477	1	US-08-444-734A-4	Sequence 4, Appl
48	7	2.2	477	1	US-08-087-772A-16	Sequence 16, Appl
49	7	2.2	660	3	US-09-111-085-2	Sequence 2, Appl
50	7	2.2	660	4	US-09-376-781-5	Sequence 5, Appl

ALIGNMENTS

```
RESULT 1
US-08-842-842-7

; Sequence 7, Application US/08842842
; Patent No. 5843678
; GENERAL INFORMATION:
;  APPLICANT: Boyle, William J.
;  TITLE OF INVENTION: OSTEOPROTEGERIN BINDING PROTEINS
;  NUMBER OF SEQUENCES: 7
;  CORRESPONDENCE ADDRESS:
;    ADDRESSEE: Amgen Inc.
;    STREET: 1840 Dehavilland Drive
;    CITY: Thousand Oaks
;    STATE: California
;    COUNTRY: USA
;    ZIP: 91230-1789
;  COMPUTER READABLE FORM:
;    MEDIUM TYPE: Floppy disk
;    COMPUTER: IBM PC compatible
;    OPERATING SYSTEM: PC-DOS/MS-DOS
;    SOFTWARE: PatentIn Release #1.0, Version #1.30
;  CURRENT APPLICATION DATA:
;    APPLICATION NUMBER: US/08/842,842
;    FILING DATE:
;    CLASSIFICATION: 435
;  ATTORNEY/AGENT INFORMATION:
;    NAME: Winter, Robert B.
;    REFERENCE/DOCKET NUMBER: A-451
;  INFORMATION FOR SEQ ID NO: 7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH: 316 amino acids
;      TYPE: amino acid
;      TOPOLOGY: linear
;    MOLECULE TYPE: protein
US-08-842-842-7

Query Match       100.0%;  Score 316;  DB 2;  Length 316;
Best Local Similarity  100.0%;  Pred. No. 0;
Matches  316;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy   1 MRRASRDYGKYLRSSEEMGSGGPGVPHEGPLHPAPSAPAPAPPPAASRSMFLALLGLGLGQ 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MRRASRDYGKYLRSSEEMGSGGPGVPHEGPLHPAPSAPAPAPPPAASRSMFLALLGLGLGQ 60

Qy  61 VVCSIALFLYFRAQMDPNRISEDSTHCFYRILRHENAGLQDSTLESEDTLPDSCRRMKQ 120
```

Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   61 VVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESEDTLPDSCRRMKQ 120
Qy 121 AFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHK 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 AFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHK 180
Qy 181 VTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVY 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 VTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVY 240
Qy 241 VVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDP 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 VVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDP 300
Qy 301 DQDATYFGAFKVQDID 316
        ||||||||||||||||
Db 301 DQDATYFGAFKVQDID 316

Query Match   100.0%;   Score 316; DB 4; Length 316;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 316; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MRRASRDYGKYLRSSEEMGSGPGVPHEGPLHPAPSAPAPPAASRMFLALLGLGLGQ 60
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MRRASRDYGKYLRSSEEMGSGPGVPHEGPLHPAPSAPAPPAASRMFLALLGLGLGQ 60

Qy   61 VVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESEDTLPDSCRRMKQ 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 VVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESEDTLPDSCRRMKQ 120
Qy 121 AFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHK 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 AFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHK 180
Qy 181 VTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVY 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 VTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVY 240
Qy 241 VVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDP 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 VVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDP 300
Qy 301 DQDATYFGAFKVQDID 316
        ||||||||||||||||
Db 301 DQDATYFGAFKVQDID 316

Query Match   100.0%;   Score 316; DB 4; Length 316;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 316; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MRRASRDYGKYLRSSEEMGSGPGVPHEGPLHPAPSAPAPPAASRMFLALLGLGLGQ 60
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MRRASRDYGKYLRSSEEMGSGPGVPHEGPLHPAPSAPAPPAASRMFLALLGLGLGQ 60
Qy   61 VVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESEDTLPDSCRRMKQ 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 VVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESEDTLPDSCRRMKQ 120
Qy 121 AFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHK 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 AFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHK 180
Qy 181 VTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVY 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 VTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVY 240
Qy 241 VVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDP 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 VVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDP 300
Qy 301 DQDATYFGAFKVQDID 316
        ||||||||||||||||
Db 301 DQDATYFGAFKVQDID 316

RESULT 4
US-08-996-139-11
; Sequence 11, Application US/08996139
; Patent No. 6017729
; GENERAL INFORMATION:
;   APPLICANT: Anderson, Dirk M.
;   APPLICANT: Galibert, Laurent
;   APPLICANT: Maraskovsky, Eugene
;   TITLE OF INVENTION: Receptor Activator of NF-kappaB
;   NUMBER OF SEQUENCES: 19
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Immunex Corporation, Law Department
;   STREET: 51 University Street
;   CITY: Seattle
;   STATE: WA
;   COUNTRY: USA
;   ZIP: 98101
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: Apple Power Macintosh
;   OPERATING SYSTEM: Apple Operating System 7.5.5
;   SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/996,139
;   FILING DATE: 22 DECEMBER 1997
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: USSN 60/064,671
;   FILING DATE: 14 OCTOBER 1997
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: USSN 08/813,509
;   FILING DATE: 07 MARCH 1997
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: USSN 08/772,330
;   FILING DATE: 23 DECEMBER 1996
;   CLASSIFICATION:
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Perkins, Patricia Anne
;   REGISTRATION NUMBER: 34,693
;   REFERENCE/DOCKET NUMBER: 2851-A
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (206)587-0430
;   TELEFAX: (206)233-0644
;   INFORMATION FOR SEQ ID NO: 11:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 294 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-996-139-11

Query Match   68.7%; Score 217; DB 3; Length 294;
Best Local Similarity 100.0%; Pred. No. 6.7e-210;
Matches 217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   100 LQDSTLESEDTLPDSCRRMKQAFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKP 159
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   78 LQDSTLESEDTLPDSCRRMKQAFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKP 137

Qy   160 EAQPFAHLTINAASIPSGSHKVTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANI 219
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   138 EAQPFAHLTINAASIPSGSHKVTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANI 197

Qy   220 CFRHHETSGSVPTDYLQLMYVVVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGF 279
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   198 CFRHHETSGSVPTDYLQLMYVVVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGF 257

Qy   280 FKLRAGEEISIQVSNPSLLDPDQDATYFGAFKVQDID 316
             ||||||||||||||||||||||||||||||||||||
Db   258 FKLRAGEEISIQVSNPSLLDPDQDATYFGAFKVQDID 294

RESULT 5
US-08-995-659-11
; Sequence 11, Application US/08995559
; Patent No. 6242213
; GENERAL INFORMATION:
;   APPLICANT: Anderson, Dirk M.
;   APPLICANT: Galibert, Laurent
;   APPLICANT: Maraskovsky, Eugene
;   TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
;   NUMBER OF SEQUENCES: 19
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Immunex Corporation, Law Department
;   STREET: 51 University Street
;   CITY: Seattle
;   STATE: WA
;   COUNTRY: USA
;   ZIP: 98101
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: Apple Power Macintosh
;   OPERATING SYSTEM: Apple Operating System 7.5.5
;   SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/995,659
;   FILING DATE: 22 DECEMBER 1997
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: USSN 60/064,671
;   FILING DATE: 14 OCTOBER 1997
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: USSN 08/813,509
;   FILING DATE: 07 MARCH 1997
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: USSN 08/772,330
;   FILING DATE: 23 DECEMBER 1996
;   CLASSIFICATION:
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Perkins, Patricia Anne
;   REGISTRATION NUMBER: 34,693
;   REFERENCE/DOCKET NUMBER: 2852-A
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (206)587-0430
;   TELEFAX: (206)233-0644
;   INFORMATION FOR SEQ ID NO: 11:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 294 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-995-659-11

Query Match   68.7%; Score 217; DB 4; Length 294;
Best Local Similarity 100.0%; Pred. No. 6.7e-210;
Matches 217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   100 LQDSTLESEDTLPDSCRRMKQAFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKP 159
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   78 LQDSTLESEDTLPDSCRRMKQAFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKP 137

Qy   160 EAQPFAHLTINAASIPSGSHKVTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANI 219
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   138 EAQPFAHLTINAASIPSGSHKVTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANI 197

Qy   220 CFRHHETSGSVPTDYLQLMYVVVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGF 279
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   198 CFRHHETSGSVPTDYLQLMYVVVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGF 257

Qy   280 FKLRAGEEISIQVSNPSLLDPDQDATYFGAFKVQDID 316
             ||||||||||||||||||||||||||||||||||||
Db   258 FKLRAGEEISIQVSNPSLLDPDQDATYFGAFKVQDID 294

RESULT 6
US-09-215-649A-11
; Sequence 11, Application US/09215649A
; Patent No. 6271349
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; Galibert, Laurent
; Maraskovsky, Eugene
; TITLE OF INVENTION: Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/215,649A
; FILING DATE: 17-Dec-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/996,139
; FILING DATE: <Unknown>
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2851-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 294 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-215-649A-11

Query Match   68.7%; Score 217; DB 4; Length 294;
Best Local Similarity 100.0%; Pred. No. 6.7e-210;
Matches 217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 100 LQDSTLESEDTLPDSCRRMKQAFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKP 159
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   78 LQDSTLESEDTLPDSCRRMKQAFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKP 137

Qy 160 EAQPFAHLTINAASIPSGSHKVTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANI 219
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 138 EAQPFAHLTINAASIPSGSHKVTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANI 197

Qy 220 CFRHHETSGSVPTDYLQLMVYVVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGF 279
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 198 CFRHHETSGSVPTDYLQLMVYVVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGF 257

Qy 280 FKLRAGEISIQVSNPSLLDPDQDATYFGAFKVQDID 316
        |||||||||||||||||||||||||||||||||||
Db 258 FKLRAGEISIQVSNPSLLDPDQDATYFGAFKVQDID 294

RESULT 7

US-09-052-521C-34
; Sequence 34, Application US/09052521C
; Patent No. 6316408
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; TITLE OF INVENTION: Osteoprotegerin Binding Proteins and Receptors
; FILE REFERENCE: A-451Brv
; CURRENT APPLICATION NUMBER: US/09/052,521C
; CURRENT FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 08/880,855
; PRIOR FILING DATE: 1997-06-23
; PRIOR APPLICATION NUMBER: 08/842,842
; PRIOR FILING DATE: 1997-04-16
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Oligonucleotide
US-09-052-521C-34

Query Match   8.5%; Score 27; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.1e-20;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 170 NAASIPSGSHKVTLSSWYHDRGWAKIS 196
        ||||||||||||||||||||||||||||
Db   1 NAASIPSGSHKVTLSSWYHDRGWAKIS 27

RESULT 8
US-09-052-521C-33
; Sequence 33, Application US/09052521C
; Patent No. 6316408
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; TITLE OF INVENTION: Osteoprotegerin Binding Proteins and Receptors
; FILE REFERENCE: A-451Brv
; CURRENT APPLICATION NUMBER: US/09/052,521C
; CURRENT FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 08/880,855
; PRIOR FILING DATE: 1997-06-23
; PRIOR APPLICATION NUMBER: 08/842,842
; PRIOR FILING DATE: 1997-04-16
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-052-521C-33

Query Match   7.0%; Score 22; DB 4; Length 27;
Best Local Similarity 100.0%; Pred. No. 4.1e-15;
Matches 22; Conservative 0; Mismatches 0; Indels 15; Gaps 0;

Qy 170 NAASIPSGSHKVTLSSWYHDRG 191
        |||||||||||||||||||||
Db   1 NAASIPSGSHKVTLSSWYHDRG 22

RESULT 9
US-08-996-139-13
; Sequence 13, Application US/08896139
; Patent No. 6017729

```
;  GENERAL INFORMATION:
;    APPLICANT: Anderson, Dirk M.
;    APPLICANT: Galibert, Laurent
;    APPLICANT: Maraskovsky, Eugene
;    TITLE OF INVENTION: Receptor Activator of NF-kappaB
;    NUMBER OF SEQUENCES: 19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE: Immunex Corporation, Law Department
;      STREET: 51 University Street
;      CITY: Seattle
;      STATE: WA
;      COUNTRY: USA
;      ZIP: 98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE: Floppy disk
;      COMPUTER: Apple Power Macintosh
;      OPERATING SYSTEM: Apple Operating System 7.5.5
;      SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/08/996,139
;      FILING DATE: 22 DECEMBER 1997
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: USSN 60/064,671
;      FILING DATE: 14 OCTOBER 1997
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: USSN 08/813,509
;      FILING DATE: 07 MARCH 1997
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: USSN 08/772,330
;      FILING DATE: 23 DECEMBER 1996
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME: Perkins, Patricia Anne
;      REGISTRATION NUMBER: 34,693
;      REFERENCE/DOCKET NUMBER: 2851-A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE: (206)587-0430
;      TELEFAX: (206)233-0644
;  INFORMATION FOR SEQ ID NO: 13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH: 317 amino acids
;      TYPE: amino acid
;      TOPOLOGY: linear
;      MOLECULE TYPE: protein
US-08-996-139-13

Query Match       7.0%;     Score 22;  DB 3;  Length 317;
est Local Similarity  100.0%;   Pred. No. 4.3e-14;
atches  22;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy   207  VNQDGFYYLYANICFRHHETSG  228
          ||||||||||||||||||||||
Db   208  VNQDGFYYLYANICFRHHETSG  229

RESULT 10
US-08-995-659-13
; Sequence 13, Application US/08995659
; Patent No. 6242213
;  GENERAL INFORMATION:
;    APPLICANT: Anderson, Dirk M.
;    APPLICANT: Galibert, Laurent
;    APPLICANT: Maraskovsky, Eugene
;    TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
;    NUMBER OF SEQUENCES: 19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE: Immunex Corporation, Law Department
;      STREET: 51 University Street
;      CITY: Seattle
;      STATE: WA
;      COUNTRY: USA
;      ZIP: 98101
```

```
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE: Floppy disk
;      COMPUTER: Apple Power Macintosh
;      OPERATING SYSTEM: Apple Operating System 7.5.5
;      SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/08/995,659
;      FILING DATE: 22 DECEMBER 1997
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: USSN 60/064,671
;      FILING DATE: 14 OCTOBER 1997
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: USSN 08/813,509
;      FILING DATE: 07 MARCH 1997
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: USSN 08/772,330
;      FILING DATE: 23 DECEMBER 1996
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME: Perkins, Patricia Anne
;      REGISTRATION NUMBER: 34,693
;      REFERENCE/DOCKET NUMBER: 2852-A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE: (206)587-0430
;      TELEFAX: (206)233-0644
;  INFORMATION FOR SEQ ID NO: 13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH: 317 amino acids
;      TYPE: amino acid
;      TOPOLOGY: linear
;      MOLECULE TYPE: protein
US-08-995-659-13

Query Match       7.0%;     Score 22;  DB 4;  Length 317;
Best Local Similarity  100.0%;   Pred. No. 4.3e-14;
Matches  22;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy   207  VNQDGFYYLYANICFRHHETSG  228
          ||||||||||||||||||||||
Db   208  VNQDGFYYLYANICFRHHETSG  229

RESULT 11
US-09-215-649A-13
; Sequence 13, Application US/09215649A
; Patent No. 6271349
;  GENERAL INFORMATION:
;    APPLICANT: Anderson, Dirk M.
;      Galibert, Laurent
;      Maraskovsky, Eugene
;    TITLE OF INVENTION: Receptor Activator of NF-kappaB
;    NUMBER OF SEQUENCES: 19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE: Immunex Corporation, Law Department
;      STREET: 51 University Street
;      CITY: Seattle
;      STATE: WA
;      COUNTRY: USA
;      ZIP: 98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE: Floppy disk
;      COMPUTER: Apple Power Macintosh
;      OPERATING SYSTEM: Apple Operating System 7.5.5
;      SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/09/215,649A
;      FILING DATE: 17-Dec-1998
;      CLASSIFICATION: <Unknown>
;    PRIOR APPLICATION DATA:
```

; APPLICATION NUMBER: 08/996,139
; FILING DATE: <Unknown>
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2851-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 317 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
09-215-649A-13

Query Match   7.0%;   Score 22;   DB 4;   Length 317;
Best Local Similarity   100.0%;   Pred. No. 4.3e-14;
Matches 22;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

Qy   207 VNQDGFYYLYANICFRHHETSG 228
          ||||||||||||||||||||||
Db   208 VNQDGFYYLYANICFRHHETSG 229

RESULT 12
US-09-052-521C-4
; Sequence 4, Application US/09052521C
; Patent No. 6316408
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; TITLE OF INVENTION: Osteoprotegerin Binding Proteins and Receptors
; FILE REFERENCE: A-451Brv
; CURRENT APPLICATION NUMBER: US/09/052,521C
; CURRENT FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 08/880,855
; PRIOR FILING DATE: 1997-06-23
; PRIOR APPLICATION NUMBER: 08/842,842
; PRIOR FILING DATE: 1997-04-16
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; Q ID NO 4
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Human
US-09-052-521C-4

Query Match   7.0%;   Score 22;   DB 4;   Length 317;
Best Local Similarity   100.0%;   Pred. No. 4.3e-14;
Matches 22;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

Qy   207 VNQDGFYYLYANICFRHHETSG 228
          ||||||||||||||||||||||
Db   208 VNQDGFYYLYANICFRHHETSG 229

RESULT 13
US-09-052-521C-35
; Sequence 35, Application US/09052521C
; Patent No. 6316408
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; TITLE OF INVENTION: Osteoprotegerin Binding Proteins and Receptors
; FILE REFERENCE: A-451Brv
; CURRENT APPLICATION NUMBER: US/09/052,521C

; CURRENT FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 08/880,855
; PRIOR FILING DATE: 1997-06-23
; PRIOR APPLICATION NUMBER: 08/842,842
; PRIOR FILING DATE: 1997-04-16
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-052-521C-35

Query Match   5.4%;   Score 17;   DB 4;   Length 17;
Best Local Similarity   100.0%;   Pred. No. 2.8e-10;
Matches 17;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

Qy   239 VYVVKTSIKIPSSHNLM 255
          |||||||||||||||||
Db   1 VYVVKTSIKIPSSHNLM 17

RESULT 14
US-08-870-518-2
; Sequence 2, Application US/08870518
; Patent No. 5925566
; GENERAL INFORMATION:
; APPLICANT: Davis, Roger J.
; APPLICANT: Galcheva-Gargova, Zoya
; TITLE OF INVENTION: NON-ACTIVATED RECEPTOR COMPLEX
; TITLE OF INVENTION: PROTEINS AND USES THEREOF
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/870,518
; FILING DATE: 06-JUN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/019,219
; FILING DATE: 06-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Fasse, Peter J.
; REGISTRATION NUMBER: 32,983
; REFERENCE/DOCKET NUMBER: 04020/102001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 459 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-870-518-2

Query Match   2.5%;   Score 8;   DB 2;   Length 459;
Best Local Similarity   100.0%;   Pred. No. 7;

```
Matches      8;  Conservative   0;  Mismatches    0;  Indels     0;  Gaps     0;

Qy      37 PAPAPPPA 44
           |||||||
Db      20 PAPAPPPA 27

RESULT 15
US-08-804-227C-2
; Sequence 2, Application US/08804227C
; Patent No. 5876991
; GENERAL INFORMATION:
;   APPLICANT: DeHoff, Bradley S.
;   APPLICANT: Kuhstoss, Stuart A.
;   APPLICANT: Rosteck, Paul R., Jr.
;   APPLICANT: Sutton, Kimberly L.
;   TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
;   NUMBER OF SEQUENCES: 15
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: THOMAS G. PLANT 1501
;     STREET: LILLY CORPORATE CENTER
;     CITY: INDIANAPOLIS
;     STATE: IN
;     COUNTRY: USA
;     ZIP: 46285
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM Compatible
;     OPERATING SYSTEM: MS-DOS
;     SOFTWARE: ASCI(DOS) Text only
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/804,227C
;     FILING DATE: February 21, 1997
;     CLASSIFICATION: 435
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Plant, Thomas, G.
;     REGISTRATION NUMBER: 35,784
;     REFERENCE/DOCKET NUMBER: X-8231
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 317-276-2459
; INFORMATION FOR SEQ ID NO: 2:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 4472 amino acids
;     TYPE: amino acid
;     TOPOLOGY: unknown
;   MOLECULE TYPE: protein
US-08-804-227C-2

Query Match             2.5%;  Score 8;  DB 2;  Pred. No. 62;  Length 4472;
Best Local Similarity   100.0%;
Matches      8;  Conservative   0;  Mismatches    0;  Indels     0;  Gaps     0;

Qy      34 PSAPAPAP 41
           |||||||
Db    4442 PSAPAPAP 4449

RESULT 16
US-08-997-080-4
; Sequence 4, Application US/08997080
; Patent No. 5968524
; GENERAL INFORMATION:
;   APPLICANT: WATSON, JAMES D.
;   APPLICANT: TAN, PAUL L.J
;   TITLE OF INVENTION: METHODS AND COMPOUNDS FOR THE TREATMENT OF IMMUNOLOGICALLY-
;   NUMBER OF SEQUENCES: 194
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Law Offices of Ann W. Speckman
;     STREET: 2601 Elliott Avenue, Suite 4185
;     CITY: Seattle
;     STATE: WA
;     COUNTRY: USA
;     ZIP: 98121
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Diskette
;     COMPUTER: IBM Compatible
;     OPERATING SYSTEM: DOS
;     SOFTWARE: FastSEQ for Windows Version 2.0
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/997,080
;     FILING DATE:
;     CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:
;     FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Sleath, Janet
;     REGISTRATION NUMBER: 37,007
;     REFERENCE/DOCKET NUMBER: 11000.1007
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 206-269-0565
;     TELEFAX: 206-269-0563
;     TELEX:
; INFORMATION FOR SEQ ID NO: 4:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 21 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-997-080-4

Query Match             2.2%;  Score 7;  DB 2;  Length 21;
Best Local Similarity   100.0%;  Pred. No. 3.7;
Matches      7;  Conservative   0;  Mismatches    0;  Indels     0;  Gaps     0;

Qy      37 PAPAPPP 43
           |||||||
Db       2 PAPAPPP 8

RESULT 17
US-08-997-362-4
; Sequence 4, Application US/08997362
; Patent No. 5985287
; GENERAL INFORMATION:
;   APPLICANT: Tan, Paul
;   APPLICANT: Hiyama, Jun
;   APPLICANT: Visser, Elizabeth
;   APPLICANT: Skinner, Margot
;   APPLICANT: Scott, Linda
;   APPLICANT: Prestidge, Ross
;   TITLE OF INVENTION: COMPOUNDS AND METHODS FOR
;   TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
;   NUMBER OF SEQUENCES: 194
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Law Offices of Ann W. Speckman
;     STREET: 2601 Elliott Avenue, Suite 4185
;     CITY: Seattle
;     STATE: WA
;     COUNTRY: USA
;     ZIP: 98121
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Diskette
;     COMPUTER: IBM Compatible
;     OPERATING SYSTEM: DOS
;     SOFTWARE: FastSEQ for Windows Version 2.0
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/997,362
;     FILING DATE:
;     CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: U.S. Patent Application No. 5985287  08/873,970
;     FILING DATE: June 12, 1997
```

```
        APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/705,347
        FILING DATE: August 29, 1996
     ATTORNEY/AGENT INFORMATION:
        NAME: Sleath, Janet
        REGISTRATION NUMBER: 37,007
        REFERENCE/DOCKET NUMBER: 11000.1002c2
     TELECOMMUNICATION INFORMATION:
        TELEPHONE: 206-269-0565
        TELEFAX: 206-269-0563
        TELEX:
  INFORMATION FOR SEQ ID NO: 4:
     SEQUENCE CHARACTERISTICS:
        LENGTH: 21 amino acids
        TYPE: amino acid
        STRANDEDNESS: single
        TOPOLOGY: linear
        MOLECULE TYPE: protein
US-08-997-362-4

Query Match           2.2%;  Score 7;  DB 2;  Length 21;
Best Local Similarity 100.0%;  Pred. No. 3.7;
Matches    7;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy    37 PAPAPPP 43
         |||||||
Db     2 PAPAPPP 8

RESULT 18
US-08-873-970-4
; Sequence 4, Application US/08873970
; Patent No. 6001361
; GENERAL INFORMATION:
;    APPLICANT: Tan, Paul
;    APPLICANT: Hiyama, Jun
;    APPLICANT: Visser, Elizabeth
;    APPLICANT: Skinner, Margot
;    APPLICANT: Scott, Linda
;    APPLICANT: Prestidge, Ross
;    TITLE OF INVENTION: COMPOUNDS AND METHODS FOR
;    TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
;    NUMBER OF SEQUENCES: 106
;    CORRESPONDENCE ADDRESS:
;       ADDRESSEE: Law Offices of Ann W. Speckman
;       STREET: 2601 Elliott Avenue, Suite 4185
;       CITY: Seattle
;       STATE: WA
;       COUNTRY: USA
;       ZIP: 98121
;    COMPUTER READABLE FORM:
;       MEDIUM TYPE: Diskette
;       COMPUTER: IBM Compatible
;       OPERATING SYSTEM: DOS
;       SOFTWARE: FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/08/873,970
;       FILING DATE:
;       CLASSIFICATION: 435
;    PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: 08/705,347
;       FILING DATE: 29-AUG-1996
;    ATTORNEY/AGENT INFORMATION:
;       NAME: Sleath, Janet
;       REGISTRATION NUMBER: 37,007
;       REFERENCE/DOCKET NUMBER: 11000.1002c1
;    TELECOMMUNICATION INFORMATION:
;       TELEPHONE: 206-269-0565
;       TELEFAX: 206-269-0563
;       TELEX:
;  INFORMATION FOR SEQ ID NO: 4:
;     SEQUENCE CHARACTERISTICS:
;        LENGTH: 21 amino acids
;        TYPE: amino acid
;        STRANDEDNESS: single
;        TOPOLOGY: linear
;        MOLECULE TYPE: protein
US-08-873-970-4

Query Match           2.2%;  Score 7;  DB 3;  Length 21;
Best Local Similarity 100.0%;  Pred. No. 3.7;
Matches    7;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy    37 PAPAPPP 43
         |||||||
Db     2 PAPAPPP 8

RESULT 19
US-09-095-855-4
; Sequence 4, Application US/09095855
; Patent No. 6160093
; GENERAL INFORMATION:
;    APPLICANT: Tan, Paul
;    APPLICANT: Visser, Elizabeth
;    APPLICANT: Skinner, Margot
;    APPLICANT: Prestidge, Ross
;    TITLE OF INVENTION: Compounds and Methods for
;    TITLE OF INVENTION: Treatment and Diagnosis of Mycobacterial Infections
;    NUMBER OF SEQUENCES: 208
;    CORRESPONDENCE ADDRESS:
;       ADDRESSEE: Law Offices of Ann W. Speckman
;       STREET: 2601 Elliott Avenue, Suite 4185
;       CITY: Seattle
;       STATE: WA
;       COUNTRY: USA
;       ZIP: 98121
;    COMPUTER READABLE FORM:
;       MEDIUM TYPE: Diskette
;       COMPUTER: IBM Compatible
;       OPERATING SYSTEM: DOS
;       SOFTWARE: FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/09/095,855
;       FILING DATE:
;       CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: 08/705,347
;       FILING DATE: 29-AUG-1996
;       APPLICATION NUMBER: 08/873,970
;       FILING DATE: 12-JUN-1997
;       APPLICATION NUMBER: 08/997,362
;       FILING DATE: 23-DEC-1997
;    ATTORNEY/AGENT INFORMATION:
;       NAME: Sleath, Janet
;       REGISTRATION NUMBER: 37,007
;       REFERENCE/DOCKET NUMBER: 11000.1002c3
;    TELECOMUNICATION INFORMATION:
;       TELEPHONE: 206-269-0565
;       TELEFAX: 206-269-0563
;       TELEX:
;  INFORMATION FOR SEQ ID NO: 4:
;     SEQUENCE CHARACTERISTICS:
;        LENGTH: 21 amino acids
;        TYPE: amino acid
;        STRANDEDNESS: single
;        TOPOLOGY: linear
;        MOLECULE TYPE: protein
US-09-095-855-4

Query Match           2.2%;  Score 7;  DB 4;  Length 21;
Best Local Similarity 100.0%;  Pred. No. 3.7;
Matches    7;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;
```

```
Qy    37 PAPAPPP 43
         |||||||
Db     2 PAPAPPP 8

RESULT 20
US-08-705-347A-4
; Sequence 4, Application US/08705347A
; Patent No. 6284255
; GENERAL INFORMATION:
;   APPLICANT: Tan, Paul
;   APPLICANT: Hiyama, Jun
;   APPLICANT: Visser, Elizabeth
;   APPLICANT: Skinner, Margot
;   APPLICANT: Scott, Linda
;   TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
;   TITLE OF INVENTION: DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
;   NUMBER OF SEQUENCES: 55
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Speckman Picard PLLC
;     STREET: 2601 Elliott Avenue, Suite 4185
;     CITY: Seattle
;     STATE: WA
;     COUNTRY: USA
;     ZIP: 98121
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/705,347A
;     FILING DATE: 28-AUG-1996
;     CLASSIFICATION: 424
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Sleath, Janet
;     REGISTRATION NUMBER: 37,007
;     REFERENCE/DOCKET NUMBER: 11000.1002
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 206.269.0565
;     TELEFAX: 206.269.0563
; INFORMATION FOR SEQ ID NO: 4:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 21 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-705-347A-4

Query Match             2.2%;  Score 7;  DB 4;  Length 21;
Best Local Similarity  100.0%;  Pred. No. 3.7;
Matches    7;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

RESULT 21
US-09-324-542-4
; Sequence 4, Application US/09324542
; Patent No. 6328978
; GENERAL INFORMATION:
;   APPLICANT: Watson, James D.
;   APPLICANT: Tan, Paul L.J.
;   APPLICANT: Prestidge, Ross
;   TITLE OF INVENTION: Methods and Compounds for the Treatment
;   TITLE OF INVENTION: of Immunologically-Mediated Skin Disorders
;   FILE REFERENCE: 11000.1007c1
;   CURRENT APPLICATION NUMBER: US/09/324,542
;   CURRENT FILING DATE: 1999-06-02
;   EARLIER APPLICATION NUMBER: US 08/997,080
;   EARLIER FILING DATE: 1997-12-23
;   NUMBER OF SEQ ID NOS: 194
;   SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
;   LENGTH: 21
;   TYPE: PRT
;   ORGANISM: Mycobacterium vaccae
US-09-324-542-4

Qy    37 PAPAPPP 43
         |||||||
Db     2 PAPAPPP 8

Query Match             2.2%;  Score 7;  DB 4;  Length 21;
Best Local Similarity  100.0%;  Pred. No. 3.7;
Matches    7;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

RESULT 22
US-08-640-847C-3
; Sequence 3, Application US/08640847C
; Patent No. 5993865
; GENERAL INFORMATION:
;   APPLICANT: BECH, Lene M.
;   APPLICANT: SORENSEN, Steen B.
;   APPLICANT: VAAG, Pia
;   APPLICANT: MULDBJERG, Marianne
;   APPLICANT: BEENFELDT, Thorkild
;   APPLICANT: LEAH, Robert
;   APPLICANT: BREDDAM, Klaus
;   TITLE OF INVENTION: BEVERAGE AND A METHOD OF PREPARING IT
;   NUMBER OF SEQUENCES: 41
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: LADAS & PARRY
;     STREET: 26 WEST 61 STREET
;     CITY: NEW YORK
;     STATE: NY
;     ZIP: 10023
;     COUNTRY: USA
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: 3-1/4" Disk   1.44 MB
;     COMPUTER: IBM PC Compatible
;     OPERATING SYSTEM: Microsoft Windows for Workgroups 3.11
;     SOFTWARE: WordPerfect 8 for Windows
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/640,847C
;     FILING DATE: 26-JUN-1996
;     CLASSIFICATION: 426
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: PCT/DK94/00420
;     FILING DATE: 08-NOV-1994
;     APPLICATION NUMBER: DK001266/93
;     FILING DATE: 08-NOV-1993
;   ATTORNEY/AGENT INFORMATION:
;     NAME: MASS, Clifford J.
;     REGISTRATION NUMBER: 30,086
;     REFERENCE/DOCKET NUMBER: U-010781-0
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (212) 708-1890
;     TELEFAX: (212) 246-8959
;     TELEX: 233288
; INFORMATION FOR SEQ ID NO: 3:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 41 Amino Acids
;     TYPE: Amino Acids
;     TOPOLOGY: Linear
US-08-640-847C-3

Query Match             2.2%;  Score 7;  DB 2;  Length 41;
Best Local Similarity  100.0%;  Pred. No. 7.1;
```

Matches   7; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   170 NAASIPS 176
          ||||||
Db   15 NAASIPS 21

RESULT 23
US-08-640-847C-9
; Sequence 9, Application US/08640847C
; Patent No. 5993865
; GENERAL INFORMATION:
;..   APPLICANT: BECH, Lene M.
;..   APPLICANT: SORENSEN, Steen B.
;..   APPLICANT: VAAG, Pia
;..   APPLICANT: MULDBJERG, Marianne
;..   APPLICANT: BEENFELDT, Thorkild
;..   APPLICANT: LEAH, Robert
;..   APPLICANT: BREDDAM, Klaus
;..   TITLE OF INVENTION: BEVERAGE AND A METHOD OF PREPARING IT
;..   NUMBER OF SEQUENCES: 41
;..   CORRESPONDENCE ADDRESS:
;..   ADDRESSEE: LADAS & PARRY
;..   STREET: 26 WEST 61 STREET
;..   CITY: NEW YORK
;..   STATE: NY
;..   ZIP: 10023
;..   COUNTRY: USA
;..   COMPUTER READABLE FORM:
;..   MEDIUM TYPE: 3-1/4" Disk   1.44 MB
;..   COMPUTER: IBM PC Compatible
;..   OPERATING SYSTEM: Microsoft Windows for Workgroups 3.11
;..   SOFTWARE: WordPerfect 8 for Windows
;..   CURRENT APPLICATION DATA:
;..   APPLICATION NUMBER: US/08/640,847C
;..   FILING DATE: 26-JUN-1996
;..   CLASSIFICATION: 426
;..   PRIOR APPLICATION DATA:
;..   APPLICATION NUMBER: PCT/DK94/00420
;..   FILING DATE: 08-NOV-1994
;..   APPLICATION NUMBER: DK001266/93
;..   FILING DATE: 08-NOV-1993
;..   ATTORNEY/AGENT INFORMATION:
;..   NAME: MASS, Clifford J.
;..   REGISTRATION NUMBER: 30,086
;..   REFERENCE/DOCKET NUMBER: U-010781-0
;..   TELECOMMUNICATION INFORMATION:
;..   TELEPHONE: (212) 708-1890
;..   TELEFAX: (212) 246-8959
;..   TELEX: 233288
;..   INFORMATION FOR SEQ ID NO: 9:
;..   SEQUENCE CHARACTERISTICS:
;..   LENGTH: 41 Amino Acids
;..   TYPE: Amino Acids
;..   TOPOLOGY: Linear
US-08-640-847C-9

Query Match   2.2%; Score 7; DB 2; Length 41;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches   7; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   170 NAASIPS 176
          ||||||
Db   15 NAASIPS 21

RESULT 24
US-08-640-847C-12
; Sequence 12, Application US/08640847C
; Patent No. 5993865
; GENERAL INFORMATION:
;..   APPLICANT: BECH, Lene M.

;..   APPLICANT: SORENSEN, Steen B.
;..   APPLICANT: VAAG, Pia
;..   APPLICANT: MULDBJERG, Marianne
;..   APPLICANT: BEENFELDT, Thorkild
;..   APPLICANT: LEAH, Robert
;..   APPLICANT: BREDDAM, Klaus
;..   TITLE OF INVENTION: BEVERAGE AND A METHOD OF PREPARING IT
;..   NUMBER OF SEQUENCES: 41
;..   CORRESPONDENCE ADDRESS:
;..   ADDRESSEE: LADAS & PARRY
;..   STREET: 26 WEST 61 STREET
;..   CITY: NEW YORK
;..   STATE: NY
;..   ZIP: 10023
;..   COUNTRY: USA
;..   COMPUTER READABLE FORM:
;..   MEDIUM TYPE: 3-1/4" Disk   1.44 MB
;..   COMPUTER: IBM PC Compatible
;..   OPERATING SYSTEM: Microsoft Windows for Workgroups 3.11
;..   SOFTWARE: WordPerfect 8 for Windows
;..   CURRENT APPLICATION DATA:
;..   APPLICATION NUMBER: US/08/640,847C
;..   FILING DATE: 26-JUN-1996
;..   CLASSIFICATION: 426
;..   PRIOR APPLICATION DATA:
;..   APPLICATION NUMBER: PCT/DK94/00420
;..   FILING DATE: 08-NOV-1994
;..   APPLICATION NUMBER: DK001266/93
;..   FILING DATE: 08-NOV-1993
;..   ATTORNEY/AGENT INFORMATION:
;..   NAME: MASS, Clifford J.
;..   REGISTRATION NUMBER: 30,086
;..   REFERENCE/DOCKET NUMBER: U-010781-0
;..   TELECOMMUNICATION INFORMATION:
;..   TELEPHONE: (212) 708-1890
;..   TELEFAX: (212) 246-8959
;..   TELEX: 233288
;..   INFORMATION FOR SEQ ID NO: 12:
;..   SEQUENCE CHARACTERISTICS:
;..   LENGTH: 41 Amino Acids
;..   TYPE: Amino Acids
;..   TOPOLOGY: Linear
US-08-640-847C-12

Query Match   2.2%; Score 7; DB 2; Length 41;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches   7; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   170 NAASIPS 176
          ||||||
Db   15 NAASIPS 21

RESULT 25
US-08-284-391B-35
; Sequence 35, Application US/08284391B
; Patent No. 5851828
; GENERAL INFORMATION:
;..   APPLICANT: Seed, Brian
;..   APPLICANT: Banapour, Babak
;..   APPLICANT: Romeo, Charles
;..   APPLICANT: Kolanus, Waldemar
;..   TITLE OF INVENTION: TARGETED CYTOLYSIS OF HIV-INFECTED
;..   TITLE OF INVENTION: CELLS BY CHIMERIC CD4 RECEPTOR- BEARING CELLS
;..   NUMBER OF SEQUENCES: 53
;..   CORRESPONDENCE ADDRESS:
;..   ADDRESSEE: Clark & Elbing LLP
;..   STREET: 176 Federal Street
;..   CITY: Boston
;..   STATE: MA
;..   COUNTRY: USA
;..   ZIP: 02110

```
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Diskette
;     COMPUTER: IBM Compatible
;     OPERATING SYSTEM: DOS
;     SOFTWARE: FastSEQ for Windows Version 2.0
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/284,391B
;     FILING DATE: 02-AUG-1994
;     CLASSIFICATION: 514
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: 08/195,395
;     FILING DATE: 14-FEB-1994
;     APPLICATION NUMBER: 07/847,566
;     FILING DATE: 06-MAR-1992
;     APPLICATION NUMBER: 07/665,961
;     FILING DATE: 07-MAR-1991
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Elbing, Karen L
;     REGISTRATION NUMBER: 35,238
;   REFERENCE/DOCKET NUMBER: 00786/247001
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 617-428-0200
;     TELEFAX: 617-428-7045
;     TELEX:
US-08-284-391B-35

; INFORMATION FOR SEQ ID NO: 35:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 58 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;   MOLECULE TYPE: Protein
US-08-284-391B-35


Query Match     2.3%;     Score 7;  DB 2;  Length 58;
Best Local Similarity 100.0%;  Pred. No. 9.9;
Matches   7;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    53 LLGLGLG 59
         |||||||
Db    43 LLGLGLG 49


RESULT 26
US-09-218-950-35
; Sequence 35, Application US/09218950
; Patent No. 6284240
; GENERAL INFORMATION:
;   APPLICANT: Seed, Brian
;   APPLICANT: Banapour, Babak
;   APPLICANT: Romeo, Charles
;   APPLICANT: Kolanus, Waldemar
;   TITLE OF INVENTION: TARGETED CYTOLYSIS OF HIV-INFECTED
;   TITLE OF INVENTION: CELLS BY CHIMERIC CD4 RECEPTOR- BEARING CELLS
;   NUMBER OF SEQUENCES: 53
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Clark & Elbing LLP
;     STREET: 176 Federal Street
;     CITY: Boston
;     STATE: MA
;     COUNTRY: USA
;     ZIP: 02110
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Diskette
;     COMPUTER: IBM Compatible
;     OPERATING SYSTEM: DOS
;     SOFTWARE: FastSEQ for Windows Version 2.0
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/09/218,950
;     FILING DATE:
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US/08/284,391
```

```
;     FILING DATE: 02-AUG-1994
;     APPLICATION NUMBER: 08/195,395
;     FILING DATE: 14-FEB-1994
;     APPLICATION NUMBER: 07/847,566
;     FILING DATE: 06-MAR-1992
;     APPLICATION NUMBER: 07/665,961
;     FILING DATE: 07-MAR-1991
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Elbing, Karen L
;     REGISTRATION NUMBER: 35,238
;   REFERENCE/DOCKET NUMBER: 00786/247001
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 617-428-0200
;     TELEFAX: 617-428-7045
;     TELEX:
; INFORMATION FOR SEQ ID NO: 35:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 58 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-09-218-950-35


Query Match     2.3%;     Score 7;  DB 4;  Length 58;
Best Local Similarity 100.0%;  Pred. No. 9.9;
Matches   7;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    53 LLGLGLG 59
         |||||||
Db    43 LLGLGLG 49


RESULT 27
US-08-591-498-10
; Sequence 10, Application US/08591498
; Patent No. 5773694
; GENERAL INFORMATION:
;   APPLICANT: BROEKAERT, WILLEM F.
;   APPLICANT: CAMMUE, BRUNO P.A.
;   APPLICANT: REES, SARAH B.
;   TITLE OF INVENTION: ANTIMICROBIAL PROTEINS
;   NUMBER OF SEQUENCES: 25
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: CUSHMAN DARBY & CUSHMAN
;     ADDRESSEE: Intellectual Property Group of
;     ADDRESSEE: PILLSBURY MADISON & SUTRO LLP
;     STREET: 1100 New York Avenue, N.W.
;     CITY: Washington
;     STATE: D.C.
;     COUNTRY: U.S.A.
;     ZIP: 20005-3918
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/591,498
;     FILING DATE: 25-JAN-1996
;     CLASSIFICATION: 800
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: PCT/GB94/01636
;     FILING DATE: 29-JUL-1994
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: GB 9317816.8
;     FILING DATE: 27-AUG-1993
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: GB 9316158.6
;     FILING DATE: 04-AUG-1993
; INFORMATION FOR SEQ ID NO: 10:
;   SEQUENCE CHARACTERISTICS:
```

```
        LENGTH:  93 amino acids
        TYPE: amino acid
        STRANDEDNESS: single
        TOPOLOGY: linear
        MOLECULE TYPE: protein
        ORIGINAL SOURCE: PAPI
US-08-591-498-10

Query Match.            2.2%;  Score 7;  DB 1;  Length 93;
Best Local Similarity 100.0%;  Pred. No.15;
Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   170 NAASIPS 176
         |||||||
Db    67 NAASIPS 73


RESULT 28
US-08-591-498-14
Sequence 14, Application US/08591498
Patent No. 5773694
GENERAL INFORMATION:
        APPLICANT: BROEKAERT, WILLEM F.
        APPLICANT: CAMMUE, BRUNO P.A.
        APPLICANT: REES, SARAH B.
        TITLE OF INVENTION: ANTIMICROBIAL PROTEINS
        NUMBER OF SEQUENCES: 25
        CORRESPONDENCE ADDRESS:
        ADDRESSEE: CUSHMAN DARBY & CUSHMAN
        ADDRESSEE: Intellectual Property Group of
        ADDRESSEE: PILLSBURY MADISON & SUTRO LLP
        STREET: 1100 New York Avenue, N.W.
        CITY: Washington
        STATE: D.C.
        COUNTRY: U.S.A.
        ZIP: 20005-3918
        COMPUTER READABLE FORM:
        MEDIUM TYPE: Floppy disk
        COMPUTER: IBM PC compatible
        OPERATING SYSTEM: PC-DOS/MS-DOS
        SOFTWARE: PatentIn Release #1.0, Version #1.25
        CURRENT APPLICATION DATA:
        APPLICATION NUMBER: US/08/591,498
        FILING DATE: 25-JAN-1996
        CLASSIFICATION: 800
        PRIOR APPLICATION DATA:
        APPLICATION NUMBER: PCT/GB94/01636
        FILING DATE: 29-JUL-1994
        PRIOR APPLICATION DATA:
        APPLICATION NUMBER: GB 9317816.8
        FILING DATE: 27-AUG-1993
        PRIOR APPLICATION DATA:
        APPLICATION NUMBER: GB 9316158.6
        FILING DATE: 04-AUG-1993
        INFORMATION FOR SEQ ID NO: 14:
        SEQUENCE CHARACTERISTICS:
        LENGTH: 93 amino acids
        TYPE: amino acid
        STRANDEDNESS: single
        TOPOLOGY: linear
        MOLECULE TYPE: protein
        ORIGINAL SOURCE: Zm-nsLTP
US-08-591-498-14

Query Match             2.2%;  Score 7;  DB 1;  Length 93;
Best Local Similarity 100.0%;  Pred. No.15;
Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   170 NAASIPS 176
```

```
                                                     |||||||
Db    67 NAASIPS 73


RESULT 29
US-08-702-609A-4
Sequence 4, Application US/08702609A
Patent No. 6031152
GENERAL INFORMATION:
        APPLICANT: Olsen, Odd-Arne
        APPLICANT: Kalla, Roger
        APPLICANT: Linnestad, Casper
        TITLE OF INVENTION: Promoter from a Lipid
        TITLE OF INVENTION: Transfer Protein Gene
        NUMBER OF SEQUENCES: 6
        CORRESPONDENCE ADDRESS:
        ADDRESSEE: Plant Molecular Biology Laboratory,
        ADDRESSEE: Department of Biotechnical Sciences, Agricultural
        ADDRESSEE: University of No. 6031152way and Agricultural Biotechnology
        ADDRESSEE: Program NRC
        COUNTRY: No. 6031152way
        ZIP: N-1432
        COMPUTER READABLE FORM:
        MEDIUM TYPE: 3.5" 1.44 Mb diskette
        COMPUTER: IBM PC
        OPERATING SYSTEM: WINDOWS 98
        SOFTWARE: Word Processing
        CURRENT APPLICATION DATA:
        APPLICATION NUMBER: US/08/702,609A
        FILING DATE: 20-NOV-1996
        CLASSIFICATION: 435
        PRIOR APPLICATION DATA:
        APPLICATION NUMBER: PCTNO95\00042
        FILING DATE: 23.02.95
        ATTORNEY/AGENT INFORMATION:
        NAME: Thaddius J. Carvis
        REGISTRATION NUMBER: 26110
        REFERENCE/DOCKET NUMBER: 833-P0016A
        TELECOMMUNICATION INFORMATION:
        TELEPHONE: 203-324-6155
        TELEFAX: 203-327-1096
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
        LENGTH: 117 residues
        TYPE: amino acid
        STRANDEDNESS: double
        TOPOLOGY: linear
        MOLECULE TYPE:
        ORIGINAL SOURCE:
        ORGANISM: Barley
        PUBLICATION INFORMATION:
        AUTHORS: Linnestad, Casper
        AUTHORS: Lonneborg, Anders
        AUTHORS: Kalla, Roger
        AUTHORS: Olsen, Odd-Arne
        TITLE: Promoter of a Lipid Transfer Protein Gene
        TITLE: Expressed in Barley Aleurone Cells Contains
        TITLE: Similar myb and myc Recognition Sites as the Maize
        TITLE: Bz-McC Allele
        JOURNAL: Plant Physiol.
        VOLUME: 97
        PAGES: 842
        DATE: 17.06.91
US-08-702-609A-4


Query Match             2.2%;  Score 7;  DB 3;  Length 117;
Best Local Similarity 100.0%;  Pred. No.19;
Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   170 NAASIPS 176
         |||||||
```

Db   91 NAASIPS 97

RESULT 30
US-08-702-609A-6
; Sequence 6, Application US/08702609A
; Patent No. 6031152
; GENERAL INFORMATION:
;   APPLICANT: Olsen, Odd-Arne
;   APPLICANT: Kalla, Roger
;   APPLICANT: Linnestad, Casper
;   TITLE OF INVENTION: Promoter from a Lipid
;   TITLE OF INVENTION: Transfer Protein Gene
;   NUMBER OF SEQUENCES: 6
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Plant Molecular Biology Laboratory, Agricultural
;   ADDRESSEE: Department of Biotechnical Sciences, Agricultural
;   ADDRESSEE: University of No. 6031152way and Agricultural Biotechnology
;   ADDRESSEE: Program NRC
;   COUNTRY: No. 6031152way
;   ZIP: N-1432
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: 3.5" 1.44 Mb diskette
;   COMPUTER: IBM PC
;   OPERATING SYSTEM: WINDOWS 98
;   SOFTWARE: Word Processing
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/702,609A
;   FILING DATE: 20-NOV-1996
;   CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: PCT\NO95\00042
;   FILING DATE: 23.02.95
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Thaddius J. Carvis
;   REGISTRATION NUMBER: 26110
;   REFERENCE/DOCKET NUMBER: 833-P0016A
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 203-324-6155
;   TELEFAX: 203-327-1096
; INFORMATION FOR SEQ ID NO: 6:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 117 residues
;   TYPE: amino acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
;   MOLECULE TYPE:
;   ORIGINAL SOURCE:
;   ORGANISM: Barley
;   PUBLICATION INFORMATION:
;   AUTHORS:
;   AUTHORS: Skriver, Karen
;   AUTHORS: Leah, Robert
;   AUTHORS: Muller-Uri, Frieder
;   AUTHORS: Olsen, Finn-Lok
;   AUTHORS: Mundy, John
;   TITLE: Structure and Expression of the Barley Lipid Transfer Protein Promoter of
;   JOURNAL: Plant Molecular Biology
;   VOLUME: 18
;   PAGES: 587
;   DATE: 16.09.91
US-08-702-609A-6

Query Match   2.2%; Score 7; DB 3; Length 117;
Best Local Similarity   100.0%; Pred. No. 19;
Matches   7; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   170 NAASIPS 176
          |||||||
Db   91 NAASIPS 97

RESULT 31
US-08-799-149C-3
; Sequence 3, Application US/08799149C
; Patent No. 6008195
; GENERAL INFORMATION:
;   APPLICANT: Michael E. Selsted
;   TITLE OF INVENTION: Antimicrobial Peptides and
;   TITLE OF INVENTION: Methods of Use
;   NUMBER OF SEQUENCES: 7
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Fish & Richardson, P.C.
;   STREET: 4225 Executive Square, Suite 1400
;   CITY: La Jolla
;   STATE: CA
;   COUNTRY: USA
;   ZIP: 92037
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette
;   COMPUTER: IBM Compatible
;   OPERATING SYSTEM: Windows95
;   SOFTWARE: FastSEQ for Windows Version 2.0
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/799,149C
;   FILING DATE: 14-February-1997
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 60/011,834
;   FILING DATE: 16-February-1996
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Lisa A. Haile, Ph.D.
;   REGISTRATION NUMBER: 38,347
;   REFERENCE/DOCKET NUMBER: 07306/009001
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 619/678-5070
;   TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 3:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 190 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
;   FEATURE:
;   NAME/KEY: Coding Sequence
;   LOCATION: 39..598
US-08-799-149C-3

Query Match   2.2%; Score 7; DB 3; Length 190;
Best Local Similarity   100.0%; Pred. No. 31;
Matches   7; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   51 LALLGLG 57
         |||||||
Db   13 LALLGLG 19

RESULT 32
US-09-199-637A-211
; Sequence 211, Application US/09199637A
; Patent No. 6355411
; GENERAL INFORMATION:
;   APPLICANT: Ausubel, Frederick
;   APPLICANT: Goodman, Howard M.
;   APPLICANT: Rahme, Laurence G.
;   APPLICANT: Mahajan-Miklos, Shalina
;   APPLICANT: Tan, Man-Wah
;   APPLICANT: Cao, Hui
;   APPLICANT: Drenkard, Eliana
;   APPLICANT: Tsongalis, John
;   TITLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC ACID
;   TITLE OF INVENTION: SEQUENCES AND USES THEREOF
;   FILE REFERENCE: 00786/361002
;   CURRENT APPLICATION NUMBER: US/09/199,637A
;   CURRENT FILING DATE: 1998-11-25

;   PRIOR APPLICATION NUMBER: 60/066,517
;   PRIOR FILING DATE: 1997-11-25
;   NUMBER OF SEQ ID NOS: 437
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 211
;   LENGTH: 207
;   TYPE: PRT
;   ORGANISM: Pseudomonas aeruginosa
US-09-199-637A-211

Query Match   2.2%;   Score 7;   DB 4;   Length 207;
Best Local Similarity   100.0%;   Pred. No. 33;
Matches   7;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   33 APSAPAP 39
          |||||||
Db   89 APSAPAP 95

RESULT 33
US-09-171-461-11
; Sequence 11, Application US/09171461
; Patent No. 6335016
; GENERAL INFORMATION:
;   APPLICANT: Baker, Adam
;   APPLICANT: Cotten, Matthew
;   APPLICANT: Chiocca, Susanna
;   APPLICANT: Kurzbauer, Robert
;   APPLICANT: Schaffner, Gotthold
;   TITLE OF INVENTION: Chicken Embryo Lethal Orphan (CELO) Virus
;   FILE REFERENCE: 0652.1800000
;   CURRENT APPLICATION NUMBER: US/09/171,461
;   CURRENT FILING DATE: 1999-01-12
;   EARLIER APPLICATION NUMBER: PCT/EP97/01944
;   EARLIER FILING DATE: 1997-04-18
;   NUMBER OF SEQ ID NOS: 54
;   SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
;   LENGTH: 223
;   TYPE: PRT
;   ORGANISM: CELO Virus
;   FEATURE:
;   OTHER INFORMATION: Position: 17559..18230 /gene: L3 /product: L3 pVI
US-09-171-461-11

Query Match   2.2%;   Score 7;   DB 4;   Length 223;
Best Local Similarity   100.0%;   Pred. No. 36;
Matches   7;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   36 APAPAPP 42
          |||||||
Db   143 APAPAPP 149

RESULT 34
US-08-420-235B-47
; Sequence 47, Application US/08420235B
; Patent No. 5801042
; GENERAL INFORMATION:
;   APPLICANT: Chang, Yuan
;   APPLICANT: Moore, Patrick S.
;   TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS
;   TITLE OF INVENTION: SEQUENCES AND USES THEREOF
;   NUMBER OF SEQUENCES: 47
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Cooper & Dunham LLP
;   STREET: 1185 Avenue of the Americas
;   CITY: New York
;   STATE: New York
;   COUNTRY: U.S.A.
;   ZIP: 10036

;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/420,235B
;   FILING DATE:
;   CLASSIFICATION: 424
;   ATTORNEY/AGENT INFORMATION:
;   NAME: White, John P.
;   REGISTRATION NUMBER: 28,678
;   REFERENCE/DOCKET NUMBER: 45185-B
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (212) 278-0400
;   TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 47:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 301 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-420-235B-47

Query Match   2.2%;   Score 7;   DB 1;   Length 301;
Best Local Similarity   100.0%;   Pred. No. 47;
Matches   7;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   55 GLGLGQV 61
          |||||||
Db   42 GLGLGQV 48

RESULT 35
US-08-343-101A-22
; Sequence 22, Application US/0834310lA
; Patent No. 5830759
; GENERAL INFORMATION:
;   APPLICANT: Chang, Yuan
;   APPLICANT: Moore, Patrick S.
;   TITLE OF INVENTION: Unique Associated Kaposi's Sarcoma
;   TITLE OF INVENTION: Virus Sequences And Uses Thereof
;   NUMBER OF SEQUENCES: 22
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Cooper & Dunham
;   STREET: 1185 Avenue of the Americas
;   CITY: New York
;   STATE: New York
;   COUNTRY: U.S.A.
;   ZIP: 10036
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.24
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/343,101A
;   FILING DATE:
;   CLASSIFICATION: 514
;   ATTORNEY/AGENT INFORMATION:
;   NAME: White Esq., John P.
;   REGISTRATION NUMBER: 28,678
;   REFERENCE/DOCKET NUMBER: 45185-A
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 212-278-0400
;   TELEFAX: 212-391-0526
; INFORMATION FOR SEQ ID NO: 22:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 301 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein

us-09-671-658a-2.oligo.rai

US-08-343-101A-22

Query Match   2.2%;   Score 7;   DB 2;   Length 301;
Best Local Similarity   100.0%;   Pred. No. 47;
Matches   7; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   55 GLGLGQV 61
         |||||||
Db   42 GLGLGQV 48

Search completed: July 15, 2002, 11:06:45
Job time: 135 sec

```
                    GenCore version 4.5
            Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on:    July 15, 2002, 11:06:51 ; Search time 13.45 Seconds
                                     (without alignments)
                                     909.694 Million cell updates/sec

Title:          US-09-671-658a-2
Perfect score:  316
Sequence:       1 MRRASRDYGKYLRSSEEMGS.........LLDPDQDATYFGAFKVQDID 316

Scoring table:  OLIGO
                Gapop 60.0 , Gapext 60.0

Searched:       105224 seqs, 38719550 residues

l size :        0

Total number of hits satisfying chosen parameters:   105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 50 summaries

Database :    SwissProt_40:*

    Pred. No. is the number of results predicted by chance to have a
    score greater than or equal to the score of the result being printed,
    and is derived by analysis of the total score distribution.
```

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	316	100.0	316	1	TN11_MOUSE	O35235 m tumor nec
2	22	7.0	317	1	TN11_HUMAN	O14788 h tumor nec
3	29	2.8	473	1	B1AR_CANFA	P79148 canis famil
4	9	2.8	633	1	PAN2_HUMAN	Q96rd6 homo sapien
5	8	2.5	173	1	HES2_HUMAN	Q9y543 homo sapien
6	8	2.5	194	1	MLEV_HUMAN	P08590 homo sapien
7	8	2.5	206	1	GPBB_HUMAN	P13224 homo sapien
8	8	2.5	208	1	GPBB_PAPCY	Q04785 papio cynoc
9	8	2.5	398	1	B3AR_FELCA	Q9tst4 felis silve
10	8	2.5	459	1	ZPR1_HUMAN	O75312 homo sapien
11	8	2.5	1193	1	DP3A_XYLFA	Q9pgu4 xylella fas
12	8	2.5	1425	1	MADI_HUMAN	O9h405 homo sapien
13	7	2.2	91	1	NULM_BRALA	O79420 branchiosto
14	7	2.2	96	1	NULM_PETMA	Q35541 petromyzon
15	7	2.2	99	1	NLT4_ORYSA	Q42976 oryza sativ
16	7	2.2	116	1	NLT1_ORYSA	P23096 oryza sativ
17	7	2.2	117	1	NLT1_HORVU	P07597 hordeum vul
18	7	2.2	117	1	NLT3_ORYSA	Q42999 oryza sativ
19	7	2.2	118	1	NLT1_SORBI	Q43193 sorghum bic
20	7	2.2	118	1	NLT2_ORYSA	Q42978 oryza sativ
21	7	2.2	120	1	NLTP_MAIZE	P19656 zea mays (m
22	7	2.2	135	1	NIU1_RHOCA	O07178 rhodobacter
23	7	2.2	198	1	PEMT_HUMAN	Q9ubm1 homo sapien
24	7	2.2	209	1	H1A_XENLA	P06892 xenopus lae
25	7	2.2	223	1	PIV6_ADEG1	O64757 avian adeno
26	7	2.2	240	1	CD7_HUMAN	P09564 homo sapien
27	7	2.2	243	1	TRIC_XENLA	P50754 xenopus lae
28	7	2.2	251	1	HXB4_HUMAN	P17483 homo sapien
29	7	2.2	267	1	LYL1_HUMAN	P12980 homo sapien
30	7	2.2	268	1	CDXL_MOUSE	P18111 mus musculu
31	7	2.2	272	1	TNR4_MOUSE	P47741 mus musculu
32	7	2.2	301	1	VP23_EBV	P25214 epstein-bar
33	7	2.2	309	1	HXB1_CHICK	P31259 gallus gall
34	7	2.2	313	1	GAG_AVISN	P03342 avian splee
35	7	2.2	337	1	NCA3_YEAST	P46955 saccharomyc
36	7	2.2	342	1	PYRC_SYNY3	P74438 synechocyst
37	7	2.2	344	1	COMC_METJA	O58820 methanococc
38	7	2.2	348	1	CEBB_BOVIN	O02755 bos taurus
39	7	2.2	354	1	PROW_SALTY	P17327 salmonella
40	7	2.2	391	1	HERP_HUMAN	O15011 homo sapien
41	7	2.2	400	1	MKK2_HUMAN	P49137 homo sapien
42	7	2.2	402	1	ODP2_MYCPN	P75392 mycoplasma
43	7	2.2	405	1	B3AR_CANFA	O02662 canis famil
44	7	2.2	407	1	G110_HUMAN	Q16186 homo sapien
45	7	2.2	407	1	G110_MOUSE	Q9jkv1 mus musculu
46	7	2.2	407	1	G110_RAT	Q9jmb5 rattus norv
47	7	2.2	408	1	BTN1_YEAST	P47040 saccharomyc
48	7	2.2	422	1	PAFA_CHICK	Q90678 g platelet-
49	7	2.2	426	1	ASD4_NEUCR	Q9hev5 neurospora
50	7	2.2	446	1	KLF5_MOUSE	Q9z0z7 mus musculu

ALIGNMENTS

```
RESULT   1
TN11_MOUSE
ID  TN11_MOUSE   STANDARD;   PRT;   316 AA.
AC  O35235; O35306;
DT  16-OCT-2001 (Rel. 40, Created)
DT  16-OCT-2001 (Rel. 40, Last sequence update)
DT  16-OCT-2001 (Rel. 40, Last annotation update)
DE  Tumor necrosis factor ligand superfamily member 11 (Receptor activator
DE  of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-
DE  induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteoclast
DE  differentiation factor) (ODF) (Osteoclastogenesis-inhibitory factor)
DE  (OCIF).
GN  TNFSF11 OR RANKL OR TRANCE OR OPGL.
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  TISSUE=Hybridoma;
RX  MEDLINE=97460112;  PubMed=9312132;
RA  Wong B.R., Rho J., Arron J., Robinson E., Orlinick J., Chao M.,
RA  Kalachikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee S.Y.,
RA  Choi Y.;
RT  "TRANCE is a novel ligand of the tumor necrosis factor receptor family
RT  that activates c-Jun N-terminal kinase in T cells.";
RL  J. Biol. Chem. 272:25190-25194(1997).
RN  [2]
RP  SEQUENCE FROM N.A.
RC  TISSUE=Bone marrow;
RX  MEDLINE=9827661; PubMed=9568710;
RA  Lacey D.L., Timms E., Tan H.-L., Kelley M.J., Dunstan C.R.,
RA  Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hsu H.,
RA  Sullivan J., Hawkins N., Davy E., Capparelli C., Eli A., Qian Y.-X.,
RA  Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J.,
RA  Boyle W.J.;
RT  "Osteoprotegerin ligand is a cytokine that regulates osteoclast
RT  differentiation and activation.";
RL  Cell 93:165-176(1998).
RN  [3]
RP  SEQUENCE FROM N.A.
RC  TISSUE=Bone marrow stroma;
RX  MEDLINE=98188248; PubMed=9520411;
RA  Yasuda H., Shima N., Nakagawa N., Yamaguchi K., Kinosaki M.,
RA  Mochizuki S.-I., Tomoyasu A., Yano K., Goto M., Murakami A., Tsuda E.,
RA  Morinaga T., Higashio K., Udagawa N., Takahashi N., Suda T.;
RT  "Osteoclast differentiation factor is a ligand for
RT  osteoprotegerin/osteoclastogenesis-inhibitory factor and is identical
RT  to TRANCE/RANKL.";
RL  Proc. Natl. Acad. Sci. U.S.A. 95:3597-3602(1998).
RN  [4]
```

```
RP   SEQUENCE FROM N.A.
RC   TISSUE=Thymic lymphoma;
RX   MEDLINE=98032977; PubMed=9367155;
RA   Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
RA   Tometsko M.E., Roux E.R., Teepe M.C., DuBose R.F., Cosman D.,
RA   Galibert L.;
RT   "A homologue of the TNF receptor and its ligand enhance T-cell growth
RT   and dendritic-cell function.";
RL   Nature 390:175-179(1997).
RN   [5]
RP   SEQUENCE FROM N.A.
RA   Ikeda T.;
RL   Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: OSTEOCLAST DIFFERENTIATION AND ACTIVATION FACTOR.
CC       AUGMENTS ABILITY OF DENDRITIC CELLS TO STIMULATE NAIVE T-CELL
CC       PROLIFERATION. MAY BE AN IMPORTANT REGULATOR OF INTERACTIONS
CC       BETWEEN T CELLS AND DENDRITIC CELLS AND MAY PLAY A ROLE IN THE
CC       REGULATION OF THE T CELL-DEPENDENT IMMUNE RESPONSE.
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
CC   -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THYMUS AND LYMPH NODES BUT
CC       NOT IN NONLYMPHOID TISSUES AND IS ABUNDANTLY EXPRESSED IN T CELLS
CC       BUT NOT IN B CELLS. A HIGH LEVEL EXPRESSION IS ALSO SEEN IN THE
CC       TRABECULAR BONE AND LUNG.
CC   -!- DISEASE: DEFICIENCY IN TNFSF11 RESULTS IN FAILURE TO FORM LOBULO-
CC       ALVEOLAR MAMMARY STRUCTURES DURING PREGNANCY, RESULTING IN DEATH
CC       OF NEWBORNS. TRANCE-DEFICIENT MICE SHOW SEVERE OSTEOPETROSIS, WITH
CC       NO OSTEOCLASTS, MARROW SPACES, OR TOOTH ERUPTION, AND EXHIBIT
CC       PROFOUND GROWTH RETARDATION AT SEVERAL SKELETAL SITES, INCLUDING
CC       THE LIMBS, SKULL, AND VERTEBRAE AND HAVE MARKED CHONDRODYSPLASIA,
CC       WITH THICK, IRREGULAR GROWTH PLATES AND A RELATIVE INCREASE IN
CC       HYPERTROPHIC CHONDROCYTES.
CC   -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; AF053713; AAC40113.1; -.
DR   EMBL; AF013170; AAC71061.1; -.
DR   EMBL; AB008426; BAA25425.1; -.
DR   EMBL; AF019048; AAB86812.1; -.
DR   EMBL; AB036798; BAA97259.1; -.
DR   MGD; MGI:1100089; Tnfsf11.
DR   InterPro; IPR003263; TNF_5.
DR   InterPro; IPR000478; TNF_family.
DR   Pfam; PF00229; TNF; 1.
DR   ProDom; PD008600; TNF_5; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; FALSE_NEG.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Differentiation; Receptor; Glycoprotein; Transmembrane;
KW   Signal-anchor.
FT   DOMAIN        1     48       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     49     69       SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)
FT                               (POTENTIAL).
FT   DOMAIN       70    316       EXTRACELLULAR (POTENTIAL).
FT   CARBOHYD    197    197       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    262    262       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CONFLICT     99     99       G -> D (IN REF. 4).
SQ   SEQUENCE   316 AA;  34944 MW;  08DF63A2BE00967A CRC64;

Query Match             100.0%;  Score 316;  DB 1;  Pred. No. 0;  Length 316;
Best Local Similarity   100.0%;
Matches  316;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1 MRRASRDYGKYLRSSEEMGSGPGVPHEGPLHPAPSAPAPPPAASRSMFLALLGLGLGLGQ 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MRRASRDYGKYLRSSEEMGSGPGVPHEGPLHPAPSAPAPPPAASRSMFLALLGLGLGLGQ 60
```

```
Qy   61 VVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESEDTLPDSCRRMKQ 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 VVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESEDTLPDSCRRMKQ 120

Qy  121 AFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHK 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 AFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHK 180

Qy  181 VTLSSWTHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVY 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 VTLSSWTHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVY 240

Qy  241 VVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDP 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 VVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDP 300

Qy  301 DQDATYFGAFKVQDID 316
          ||||||||||||||||
Db  301 DQDATYFGAFKVQDID 316


RESULT  2
TN11_HUMAN
ID   TN11_HUMAN     STANDARD;      PRT;        317 AA.
AC   O14788; O14723; Q9P2Q3;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Tumor necrosis factor ligand superfamily member 11 (Receptor activator
DE   of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-
DE   induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteoclast
DE   differentiation factor) (ODF).
GN   TNFSF11 OR RANKL OR TRANCE OR OPGL.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Bone marrow, and Peripheral blood;
RX   MEDLINE=98032977; PubMed=9367155;
RA   Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
RA   Tometsko M.E., Roux E.R., Teepe M.C., DuBose R.F., Cosman D.,
RA   Galibert L.;
RT   "A homologue of the TNF receptor and its ligand enhance T-cell growth
RT   and dendritic-cell function.";
RL   Nature 390:175-179(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymph node;
RX   MEDLINE=98227661; PubMed=9958710;
RA   Lacey D.L., Timms E., Tan H.-L., Kelley M.J., Dunstan C.R.,
RA   Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hsu H.,
RA   Sullivan J., Hawkins N., Davy E., Capparelli C., Eli A., Qian Y.-X.,
RA   Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J.,
RA   Boyle W.J.;
RT   "Osteoprotegerin ligand is a cytokine that regulates osteoclast
RT   differentiation and activation.";
RL   Cell 93:165-176(1998).
RN   [3]
RP   SEQUENCE OF 73-317 FROM N.A.
RC   TISSUE=Thymocytes;
RX   MEDLINE=97460112; PubMed=9312132;
RA   Wong B.R., Rho J., Arron J., Robinson E., Orlinick J., Chao M.,
RA   Kalachikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee S.Y.,
RA   Choi Y.;
RT   "TRANCE is a novel ligand of the tumor necrosis factor receptor family
RT   that activates c-Jun N-terminal kinase in T cells.";
RL   J. Biol. Chem. 272:25190-25194(1997).
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORM 2).
RC   TISSUE=Tongue;
```

```
RX   MEDLINE=20175237; PubMed=10708588;
RA   Nagai M., Kyakumoto S., Sato N.;
RT   "Cancer cells responsible for humoral hypercalcemia express mRNA
RT   encoding a secreted form of ODF/TRANCE that induces osteoclast
RT   formation.";
RL   Biochem. Biophys. Res. Commun. 269:532-536(2000).
CC   -!- FUNCTION: OSTEOCLAST DIFFERENTIATION AND ACTIVATION FACTOR.
CC       AUGMENTS ABILITY OF DENDRITIC CELLS TO STIMULATE NAIVE T-CELL
CC       PROLIFERATION. MAY BE AN IMPORTANT REGULATOR OF INTERACTIONS
CC       BETWEEN T CELLS AND DENDRITIC CELLS AND MAY PLAY A ROLE IN THE
CC       REGULATION OF THE T CELL-DEPENDENT IMMUNE RESPONSE. MAY ALSO PLAY
CC       AN IMPORTANT ROLE IN ENHANCED BONE-RESORPTION IN HUMORAL
CC       HYPERCALCEMIA OF MALIGNANCY.
CC   -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (ISOFORM 1) AND
CC       SECRETED (ISOFORM 2).
CC   -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2/SODF; ARE
CC       PRODUCED BY ALTERNATIVE SPLICING.
CC   -!- TISSUE SPECIFICITY: HIGHEST IN THE PERIPHERAL LYMPH NODES BUT
CC       WEAK IN SPLEEN, PERIPHERAL BLOOD LEUKOCYTES, BONE MARROW, HEART,
CC       PLACENTA, SKELETAL MUSCLE, STOMACH AND THYROID.
CC   -!- INDUCTION: UPREGULATED BY T CELL RECEPTOR STIMULATION.
CC   -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; AF019047; AAB86811.1; -.
DR   EMBL; AF053712; AAC39731.1; -.
DR   EMBL; AF013171; AAC51762.1; -.
DR   EMBL; AB037599; BAA90488.1; -.
DR   MIM; 602642; -.
DR   InterPro; IPR003263; TNF_5.
DR   InterPro; IPR000478; TNF_family.
DR   Pfam; PF00229; TNF; 1.
DR   ProDom; PD008600; TNF_5; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; FALSE_NEG.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Differentiation; Receptor; Glycoprotein; Transmembrane;
KW   Signal-anchor; Alternative splicing.
FT   DOMAIN        1     47       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     48     68       SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)
FT                                (POTENTIAL).
FT   DOMAIN       69    317       EXTRACELLULAR (POTENTIAL).
FT   CARBOHYD    171    171       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    198    198       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC      1     73       MISSING (IN ISOFORM 2).
FT   CONFLICT    194    194       A -> G (IN REF. 3).
SQ   SEQUENCE   317 AA;  35478 MW;  76617646348097F CRC64;
```

Query Match   7.0%; Score 22; DB 1; Length 317;
Best Local Similarity 100.0%; Pred. No. 1.3e-14;
Matches .22; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy 207 VNQDGFYYLYANICFRHHETSG 228
         ||||||||||||||||||||||
Db 208 VNQDGFYYLYANICFRHHETSG 229

```
RESULT 3
BIAR_CANFA
ID   BIAR_CANFA     STANDARD;     PRT;    473 AA.
AC   P79148;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUL-1998 (Rel. 36, Last annotation update)
DE   Beta-1 adrenergic receptor.
GN   ADRB1.
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=9364078; PubMed=9220370;
RA   Huang R.-R.C., Rapoport D., Schaeffer M.-T., Cascieri M.A.,
RA   Fong T.M.;
RT   "Molecular cloning of the dog beta 1 and beta 2 adrenergic
RT   receptors.";
RL   J. Recept. Signal Transduct. Res. 17:599-607(1997).
CC   -!- FUNCTION: BETA-ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
CC       INDUCED ACTIVATION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
CC       PROTEINS. THIS RECEPTOR BINDS EPINEPHRINE AND NOREPINEPHRINE WITH
CC       APPROXIMATIVELY EQUAL AFFINITY.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- PTM: HOMOLOGOUS DESENSITIZATION OF THE RECEPTOR IS MEDIATED BY ITS
CC       PHOSPHORYLATION BY BETA-ADRENERGIC RECEPTOR KINASE (BY
CC       SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; U73207; AAB93648.1; -.
DR   HSSP; P07700; 1DEP.
DR   GCRDb; GCR_1183; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein;
KW   Multigene family; Phosphorylation; Lipoprotein; Palmitate.
FT   DOMAIN        1     59       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     60     83       1 (POTENTIAL).
FT   DOMAIN       84     96       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     97    120       2 (POTENTIAL).
FT   DOMAIN      121    131       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    132    155       3 (POTENTIAL).
FT   DOMAIN      156    175       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    176    199       4 (POTENTIAL).
FT   DOMAIN      200    221       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    222    245       5 (POTENTIAL).
FT   DOMAIN      246    322       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    323    346       6 (POTENTIAL).
FT   DOMAIN      347    353       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    354    377       7 (POTENTIAL).
FT   DOMAIN      378    473       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD     15     15       N-LINKED (GLCNAC. . .) (PROBABLE).
FT   DISULFID    131    209       BY SIMILARITY.
FT   MOD_RES     309    309       PHOSPHORYLATION (BY CAPK) (POTENTIAL).
FT   LIPID       389    389       PALMITATE (BY SIMILARITY).
SQ   SEQUENCE   473 AA;  50060 MW;  361357F7DF9DBD7E CRC64;
```

Query Match   2.8%; Score 9; DB 1; Length 473;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches   9; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   36 APAPAPPPA 44
         |||||||||
Db 278 APAPAPPPA 286

RESULT 4

```
PAN2_HUMAN
ID   PAN2_HUMAN     STANDARD;      PRT;   633 AA.
AC   Q96RD6; Q96RD5; Q9UGX8;
DT   01-MAR-2002 (Rel. 41, Created)
DT   01-MAR-2002 (Rel. 41, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Pannexin 2.
GN   PANX2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RA   Baranova A., Ivanov D., Skolov M., Pestova A., Kelmanson I.,
RA   Shagin D., Usman N., Lukyanov S., Panchin Y.;
RT   "Mammalian pannexin family homologous to invertebrate gap-junction
RT   proteins are differentially expressed in nervous tissue.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20057165; PubMed=10591208;
RA   Dunham I., Hunt A.R., Collins J.E., Bruskiewich R., Beare D.M.,
RA   Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.,
RA   Bagguley C., Bailey J., Barlow K., Bates K.N., Beasley O., Bird C.P.,
RA   Blakey S., Bridgeman A.M., Buck D., Burgess J., Burrill W.D.,
RA   Burton J., Carder C., Carter N.P., Chen Y., Clark G., Clegg S.M.,
RA   Cobley V., Cole C.G., Collier R.E., Conroy R.E., Corby N., Corby N.,
RA   Coville G.J., Cox A.V., Davis J., Dawson E., Dhami P.D., Dockree C.,
RA   Dodsworth S.J., Durbin R.M., Ellington A., Evans K.L., Fey J.M.,
RA   Fleming K., French L., Garner A.A., Gilbert J.G.R., Goward M.E.,
RA   Grafham D., Griffiths M.N., Hall C., Hall R., Hall-Tamlyn C.,
RA   Heathcott R.W., Ho S., Holmes S., Hunt S.E., Jones M.C., Kershaw J.,
RA   Kimberley A., King A., Laird G.K., Langford C.F., Leversha M.A.,
RA   Lloyd C., Lloyd D.M., Martyn I.D., Mashreghi-Mohammadi M.,
RA   Matthews L., Mccann O.T., Mcclay J., Mclaren S., Mcmurray A.A.,
RA   Milne S.A., Mortimore B.J., Odell C.N., Pavitt R., Pearce A.V.,
RA   Pearson D., Phillimore B.J., Phillips S.H., Plumb R.W., Ramsay H.,
RA   Ramsey Y., Rogers L., Ross M.T., Scott C.E., Sehra H.K., Skuce C.D.,
RA   Smalley S., Smith M.L., Soderlund C., Spragon L., Steward C.A.,
RA   Sulston J.E., Swann R.M., Vaudin M., Wall R., Wallis J.M.,
RA   Whiteley M.N., Willey D., Williams L., Williams L., Williamson H.,
RA   Wilmer T.E., Wilming L., Wright C.L., Hubbard T., Bentley D.R.,
RA   Beck S., Rogers J., Shimizu N., Minoshima S., Kawasaki K., Sasaki T.,
RA   Asakawa S., Kudoh J., Shintani A., Shibuya K., Yoshizaki Y., Aoki N.,
RA   Mitsuyama S., Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S.,
RA   Do A., Do T., Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S.,
RA   Lai H., Lao H.I., Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E.,
RA   Nguyen T., Pan H., Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull S.,
RA   Sloan D., Song L., Wang Q., Wang Y., Wang Z., White J., Willingham D.,
RA   Wu H., Yao Z., Zhan M., Zhang G., Chissoe S., Murray J., Miller N.,
RA   Minx P., Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H.,
RA   Bourne S., Cordes M., Du Z., Fulton L., Goela D., Graves T.,
RA   Hawkins J., Hinds K., Kemp K., Latreille P., Layman D., Ozersky P.,
RA   Rohlfing T., Scheet P., Walker C., Wamsley A., Wohldmann P., Pepin K.,
RA   Nelson J., Korf I., Bedell J.A., Hillier L., Mardis E., Waterston R.,
RA   Wilson R., Emanuel B.S., Shaikh T., Kurahashi H., Saitta M.,
RA   Budarf M.L., McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E.,
RA   Edelmann L., Kim U.J., Shizuya H., Simon M.I., Dumanski J.P.,
RA   Peyrard M., Kedra D., Seroussi E., Fransson I., Tapia I., Bruder C.E.,
RA   O'Brien K.P., Wilkinson P., Bodenteich A., Hartman K., Hu X.,
RA   Khan A.S., Lane L., Tilahun Y., Wright H.;
RT   "The DNA sequence of human chromosome 22.";
RL   Nature 402:489-495(1999).
CC   -!- FUNCTION: STRUCTURAL COMPONENT OF THE GAP JUNCTIONS.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC   -!- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are
CC       produced by alternative splicing.
CC   -!- SIMILARITY: BELONGS TO THE INNEXIN FAMILY.
CC   -----------------------------------------------------------------------
```
```
DR   EMBL; AF398510; AAK91715.1; -.
DR   EMBL; AF398511; AAK91716.1; -.
DR   EMBL; AL022328; CAB63042.1; -.
KW   Gap junction; Transmembrane; Alternative splicing.
FT   TRANSMEM     38     60       POTENTIAL.
FT   TRANSMEM    114    136       POTENTIAL.
FT   TRANSMEM    217    239       POTENTIAL.
FT   TRANSMEM    283    305       POTENTIAL.
FT   VARSPLIC      1    124       MISSING (IN ISOFORM 2).
SQ   SEQUENCE   633 AA;  69478 MW;  C89CF833E0251D58 CRC64;

Query Match                          2.8%;
Best Local Similarity   100.0%;  Pred. No. 0.45;
Matches   9;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy    36 APAPAPPPA 44
         |||||||||
Db   486 APAPAPPPA 494


RESULT 5
HES2_HUMAN
ID   HES2_HUMAN     STANDARD;      PRT;   173 AA.
AC   Q9Y543; Q9Y542;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Transcription factor HES-2 (Hairy and enhancer of split 2).
GN   HES2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Howden P.;
RL   Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: TRANSCRIPTIONAL REPRESSOR OF GENES THAT REQUIRE A BHLH
CC       PROTEIN FOR THEIR TRANSCRIPTION (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC   -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; MAY BE
CC       PRODUCED BY ALTERNATIVE SPLICING.
CC   -!- DOMAIN: HAS A PARTICULAR TYPE OF BASIC DOMAIN (PRESENCE OF A
CC       HELIX-INTERRUPTING PROLINE) THAT BINDS TO THE N-BOX (CACNAG),
CC       RATHER THAN THE CANONICAL E-BOX (CANNTG).
CC   -!- DOMAIN: THE CARBOXYL-TERMINAL WRPW MOTIF IS A TRANSCRIPTIONAL
CC       REPRESSION DOMAIN NECESSARY FOR THE INTERACTION WITH GROUCHO, A
CC       TRANSCRIPTIONAL CO-REPRESSOR RECRUITED TO SPECIFIC TARGET DNA BY
CC       HAIRY-RELATED PROTEINS (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
CC       TRANSCRIPTION FACTORS. "HAIRY" SUBFAMILY.
CC   -----------------------------------------------------------------------
```
```
DR   EMBL; AL031848; CAB46198.1; -.
DR   EMBL; AL031848; CAB46199.1; -.
DR   InterPro; IPR003015; HLH_Myc.
DR   InterPro; IPR001092; HLH_dim.
DR   InterPro; IPR003650; Orange.
DR   Pfam; PF00010; HLH; 1.
DR   SMART; SM00353; HLH; 1.
```

```
                  GenCore version 4.5
          Copyright (c) 1993 - 2000 Compugen Ltd.

OM.protein - protein search, using sw model

Run on:      July 15, 2002, 11:01:05 ; Search time 13.12 seconds
                                   (without alignments)
                         588.299 Million cell updates/sec

Title:        US-09-671-658A-2
Perfect score: 1675
Sequence:     1 MRRASRDYGKYLRSSEEMGS.........LLDPDQDATYFGAFKVQDID 316

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched:     231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters:          231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :    Issued_Patents_AA:*
              1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
              2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
              3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
              4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
              5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
              6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

    Pred. No. is the number of results predicted by chance to have a
    score greater than or equal to the score of the result being printed,
    and is derived by analysis of the total score distribution.

                              SUMMARIES
```

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	1675	100.0	316	2	US-08-842-842-7	Sequence 7, Appli
2	1675	100.0	316	4	US-08-989-362-2	Sequence 2, Appli
3	1675	100.0	316	4	US-09-052-521C-2	Sequence 2, Appli
4	1554	92.8	294	3	US-08-996-139-11	Sequence 11, Appli
5	1554	92.8	294	4	US-08-995-659-11	Sequence 11, Appli
6	1554	92.8	294	4	US-09-215-649A-11	Sequence 11, Appli
7	1417.5	84.6	317	3	US-08-996-139-13	Sequence 13, Appli
8	1417.5	84.6	317	4	US-08-995-659-13	Sequence 13, Appli
9	1417.5	84.6	317	4	US-09-215-649A-13	Sequence 13, Appli
10	1417.5	84.6	317	4	US-09-052-521C-4	Sequence 4, Appli
11	258.5	15.4	279	4	US-09-072-993C-3	Sequence 2, Appli
12	258.5	15.4	281	1	US-08-670-354-2	Sequence 2, Appli
13	258.5	15.4	281	3	US-08-584-031-1	Sequence 1, Appli
14	258.5	15.4	281	3	US-08-780-496-1	Sequence 1, Appli
15	258.5	15.4	281	4	US-08-883-086-10	Sequence 10, Appli
16	258.5	15.4	281	4	US-09-320-424-2	Sequence 2, Appli
17	258.5	15.4	281	4	US-09-333-593A-6	Sequence 6, Appli
18	258.5	15.4	281	5	PCT-US96-10895-2	Sequence 2, Appli
19	244	14.6	291	1	US-08-670-354-6	Sequence 6, Appli
20	244	14.6	291	4	US-09-320-424-6	Sequence 6, Appli
21	244	14.6	291	5	PCT-US96-10895-6	Sequence 6, Appli
22	240	14.3	256	4	US-09-320-424-13	Sequence 13, Appli
23	236	14.1	253	4	US-09-320-424-11	Sequence 11, Appli
24	229.5	13.7	177	4	US-09-105-343A-7	Sequence 7, Appli
25	224	13.4	183	4	US-09-105-343A-8	Sequence 8, Appli
26	183	10.9	278	4	US-08-339-214-16	Sequence 16, Appli
27	183	10.9	278	4	US-08-339-214-26	Sequence 26, Appli
28	182	10.9	279	4	US-08-339-214-24	Sequence 24, Appli
29	182	10.9	279	4	US-08-339-214-32	Sequence 32, Appli
30	173.5	10.4	281	2	US-08-810-453-2	Sequence 2, Appli
31	173.5	10.4	281	3	US-08-815-190A-2	Sequence 2, Appli
32	173.5	10.4	281	4	US-09-290-640-25	Sequence 25, Appli
33	173.5	10.4	281	4	US-09-479-524-3	Sequence 3, Appli
34	173.5	10.4	281	4	US-08-339-214-8	Sequence 8, Appli
35	173.5	10.4	281	5	US-08-339-214-30	Sequence 30, Appli
36	173.5	10.4	261	5	PCT-US95-00362-2	Sequence 2, Appli
37	171.5	10.2	261	1	US-07-940-605A-2	Sequence 2, Appli
38	171.5	10.2	261	1	US-08-184-422-8	Sequence 8, Appli
39	171.5	10.2	261	1	US-08-360-923A-2	Sequence 2, Appli
40	171.5	10.2	261	2	US-08-446-922-4	Sequence 4, Appli
41	171.5	10.2	261	2	US-08-431-055-4	Sequence 4, Appli
42	171.5	10.2	261	2	US-08-690-096-2	Sequence 2, Appli
43	171.5	10.2	261	2	US-08-249-189-12	Sequence 12, Appli
44	171.5	10.2	261	2	US-08-484-624A-12	Sequence 12, Appli
45	171.5	10.2	261	2	US-08-477-733B-12	Sequence 12, Appli

```
                              ALIGNMENTS

RESULT   1
US-08-842-842-7
; Sequence 7, Application US/08842842
; Patent No. 5843678
; GENERAL INFORMATION:
;  APPLICANT: Boyle, William J.
;  TITLE OF INVENTION: OSTEOPROTEGERIN BINDING PROTEINS
;  NUMBER OF SEQUENCES: 7
;  CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Amgen Inc.
;   STREET: 1840 Dehavilland Drive
;   CITY: Thousand Oaks
;   STATE: California
;   COUNTRY: USA
;   ZIP: 91230-1789
;  COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;  CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/842,842
;   FILING DATE:
;   CLASSIFICATION: 435
;  ATTORNEY/AGENT INFORMATION:
;   NAME: Winter, Robert B.
;   REFERENCE/DOCKET NUMBER: A-451
;  INFORMATION FOR SEQ ID NO: 7:
;   SEQUENCE CHARACTERISTICS:
;    LENGTH: 316 amino acids
;    TYPE: amino acid
;    TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-842-842-7

Query Match             100.0%;  Score 1675;  DB 2;  Length 316;
Best Local Similarity   100.0%;  Pred. No. 2.9e-157;
Matches  316;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy    1 MRRASRDYGKYLRSSEEMGSGSPGVPHEGPLHPAPSAPAPPPAASRSMFLALLGLGLGQ 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MRRASRDYGKYLRSSEEMGSGSPGVPHEGPLHPAPSAPAPPPAASRSMFLALLGLGLGQ 60

Qy   61 VVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESEDTLPDSCRRMKQ 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 VVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESEDTLPDSCRRMKQ 120

Qy  121 AFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHK 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db  121 AFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHK 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  181 VTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVY 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 VTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVY 240
Qy  241 VVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDP 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 VVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDP 300
Qy  301 DQDATYFGAFKVQDID 316
        ||||||||||||||||
Db  301 DQDATYFGAFKVQDID 316


RESULT 2
US-08-989-362-2
; Sequence 2, Application US/08989362
; Patent No. 6242586
; GENERAL INFORMATION:
;   APPLICANT: Gorman, Daniel M.
;   APPLICANT: Mattson, Jeanine D.
;   TITLE OF INVENTION: Mammalian Cell Surface Antigens; Related
;   TITLE OF INVENTION: Reagents
;   NUMBER OF SEQUENCES: 2
;   CORRESPONDENCE ADDRESS:
;      ADDRESSEE: DNAX Research Institute
;      STREET: 901 California Avenue
;      CITY: Palo Alto
;      STATE: California
;      COUNTRY: USA
;      ZIP: 94304-1104
;   COMPUTER READABLE FORM:
;      MEDIUM TYPE: Floppy disk
;      COMPUTER: IBM PC compatible
;      OPERATING SYSTEM: PC-DOS/MS-DOS
;      SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/08/989,362
;      FILING DATE: 12-DEC-1997
;      CLASSIFICATION: 56
;   PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: US 60/032,846
;      FILING DATE: 13-DEC-1996
;   ATTORNEY/AGENT INFORMATION:
;      NAME: Ching, Edwin P.
;      REGISTRATION NUMBER: 34,090
;      REFERENCE/DOCKET NUMBER: DX0686
;   TELECOMMUNICATION INFORMATION:
;      TELEPHONE: (650)852-9196
;      TELEFAX: (650)496-1204
; INFORMATION FOR SEQ ID NO: 2:
;   SEQUENCE CHARACTERISTICS:
;      LENGTH: 316 amino acids
;      TYPE: amino acid
;      TOPOLOGY: linear
;   MOLECULE TYPE: Protein
US-08-989-362-2

Query Match             100.0%;  Score 1675;  DB 4;  Length 316;
Best Local Similarity   100.0%;  Pred. No. 2.9e-157;
Matches   316;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy    1 MRRASRDYGKYLRSSEEMGSGPGVPHEGPLHPAPSAPAPPPAASRSMFLALLGLGLGQ 60
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MRRASRDYGKYLRSSEEMGSGPGVPHEGPLHPAPSAPAPPPAASRSMFLALLGLGLGQ 60
Qy   61 VVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESEDTLPDSCRRMKQ 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 VVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESEDTLPDSCRRMKQ 120
Qy  121 AFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHK 180
```

```
Db  121 AFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHK 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  181 VTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVY 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 VTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVY 240
Qy  241 VVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDP 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 VVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDP 300
Qy  301 DQDATYFGAFKVQDID 316
        ||||||||||||||||
Db  301 DQDATYFGAFKVQDID 316


RESULT 3
US-09-052-521C-2
; Sequence 2, Application US/09052521C
; Patent No. 6315408
; GENERAL INFORMATION:
;   APPLICANT: Boyle, William J.
;   TITLE OF INVENTION: Osteoprotegerin Binding Proteins and Receptors
;   FILE REFERENCE: A-451Brv
;   CURRENT APPLICATION NUMBER: US/09/052,521C
;   CURRENT FILING DATE: 1998-03-30
;   PRIOR APPLICATION NUMBER: 08/880,855
;   PRIOR FILING DATE: 1997-06-23
;   PRIOR APPLICATION NUMBER: 08/842,842
;   PRIOR FILING DATE: 1997-04-16
;   NUMBER OF SEQ ID NOS: 40
;   SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 316
;   TYPE: PRT
;   ORGANISM: Mouse
US-09-052-521C-2

Query Match             100.0%;  Score 1675;  DB 4;  Length 316;
Best Local Similarity   100.0%;  Pred. No. 2.9e-157;
Matches   316;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy    1 MRRASRDYGKYLRSSEEMGSGPGVPHEGPLHPAPSAPAPPPAASRSMFLALLGLGLGQ 60
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MRRASRDYGKYLRSSEEMGSGPGVPHEGPLHPAPSAPAPPPAASRSMFLALLGLGLGQ 60
Qy   61 VVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESEDTLPDSCRRMKQ 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 VVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESEDTLPDSCRRMKQ 120
Qy  121 AFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHK 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 AFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHK 180
Qy  181 VTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVY 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 VTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVY 240
Qy  241 VVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDP 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 VVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDP 300
Qy  301 DQDATYFGAFKVQDID 316
        ||||||||||||||||
Db  301 DQDATYFGAFKVQDID 316


RESULT 4
US-08-996-139-11
; Sequence 11, Application US/08996139
; Patent No. 6017729
; GENERAL INFORMATION:
```

```
;  Sequence 11, Application US/08995659
;  Patent No. 6242213
;  GENERAL INFORMATION:
;     APPLICANT:  Anderson, Dirk M.
;     APPLICANT:  Galibert, Laurent
;     APPLICANT:  Maraskovsky, Eugene
;     TITLE OF INVENTION:  Ligand for Receptor Activator of NF-kappaB
;     NUMBER OF SEQUENCES:  19
;     CORRESPONDENCE ADDRESS:
;        ADDRESSEE:  Immunex Corporation, Law Department
;        STREET:  51 University Street
;        CITY:  Seattle
;        STATE:  WA
;        COUNTRY:  USA
;        ZIP:  98101
;     COMPUTER READABLE FORM:
;        MEDIUM TYPE:  Floppy disk
;        COMPUTER:  Apple Power Macintosh
;        OPERATING SYSTEM:  Apple Operating System 7.5.5
;        SOFTWARE:  Microsoft Word for Power Macintosh 6.0.1
;     CURRENT APPLICATION DATA:
;        APPLICATION NUMBER:  US/08/995,659
;        FILING DATE:  22 DECEMBER 1997
;        CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;        APPLICATION NUMBER:  USSN 60/064,671
;        FILING DATE:  14 OCTOBER 1997
;        CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;        APPLICATION NUMBER:  USSN 08/813,509
;        FILING DATE:  07 MARCH 1997
;        CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;        APPLICATION NUMBER:  USSN 08/772,330
;        FILING DATE:  23 DECEMBER 1996
;        CLASSIFICATION:
;     ATTORNEY/AGENT INFORMATION:
;        NAME:  Perkins, Patricia Anne
;        REGISTRATION NUMBER:  34,693
;        REFERENCE/DOCKET NUMBER:  2852-A
;     TELECOMMUNICATION INFORMATION:
;        TELEPHONE:  (206)587-0430
;        TELEFAX:   (206)233-0644
;  INFORMATION FOR SEQ ID NO:  11:
;     SEQUENCE CHARACTERISTICS:
;        LENGTH:  294 amino acids
;        TYPE:  amino acid
;        TOPOLOGY:  linear
;        MOLECULE TYPE:  protein
US-08-995-659-11

Query Match             92.8%;  Score 1554;  DB 4;  Length 294;
Best Local Similarity   99.7%;  Pred. No. 2.3e-145;
Matches  293;  Conservative   0;  Mismatches   1;  Indels   0;  Gaps   0;

Qy    23 GVPHEGPLHPAPSAPAPAPPPAASRSMFLALLGLGLGQVVCSIALFLYFRAQMDPNRISE 82
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 GVPHEGPLHPAPSAPAPAPPPAASRSMFLALLGLGLGQVVCSIALFLYFRAQMDPNRISE 60

Qy    83 DSTHCFYRILRLHENAGLQDSTLESEDTLPDSCRRMKQAFQGAVQKELQHIVGPQRFSGA 142
          ||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db    61 DSTHCFYRILRLHENADLQDSTLESEDTLPDSCRRMKQAFQGAVQKELQHIVGPQRFSGA 120

Qy   143 PAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHKVTLSSWYHDRGWAKISNMTLSN 202
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 PAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHKVTLSSWYHDRGWAKISNMTLSN 180

Qy   203 GKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVYVVKTSIKIPSSHNLMKGGSTKN 262
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVYVVKTSIKIPSSHNLMKGGSTKN 240

Qy   263 WSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKVQDID 316
```

```
US-08-996-139-11

Query Match             92.8%;  Score 1554;  DB 3;  Length 294;
Best Local Similarity   99.7%;  Pred. No. 2.3e-145;
tches  293;  Conservative   0;  Mismatches   1;  Indels   0;  Gaps   0;

Qy    23 GVPHEGPLHPAPSAPAPAPPPAASRSMFLALLGLGLGQVVCSIALFLYFRAQMDPNRISE 82
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 GVPHEGPLHPAPSAPAPAPPPAASRSMFLALLGLGLGQVVCSIALFLYFRAQMDPNRISE 60

Qy    83 DSTHCFYRILRLHENAGLQDSTLESEDTLPDSCRRMKQAFQGAVQKELQHIVGPQRFSGA 142
          ||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db    61 DSTHCFYRILRLHENADLQDSTLESEDTLPDSCRRMKQAFQGAVQKELQHIVGPQRFSGA 120

Qy   143 PAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHKVTLSSWYHDRGWAKISNMTLSN 202
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 PAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHKVTLSSWYHDRGWAKISNMTLSN 180

Qy   203 GKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVYVVKTSIKIPSSHNLMKGGSTKN 262
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVYVVKTSIKIPSSHNLMKGGSTKN 240

Qy   263 WSGNSEFHFYSINVGGFFKLRAGEISIQVSNPSLLDPDQDATYFGAFKVQDID 316
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 WSGNSEFHFYSINVGGFFKLRAGEISIQVSNPSLLDPDQDATYFGAFKVQDID 294

RESULT  5
US-08-995-659-11
```

Db　241 WSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKVQDID 294
　　　||||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 6
US-09-215-649A-11
; Sequence 11, Application US/09215649A
; Patent No. 6271349
; GENERAL INFORMATION:
;　APPLICANT: Anderson, Dirk M.
;　APPLICANT:　Galibert, Laurent
;　　　　　Maraskovsky, Eugene
;　TITLE OF INVENTION: Receptor Activator of NF-kappaB
;　NUMBER OF SEQUENCES: 19
;　CORRESPONDENCE ADDRESS:
;　　ADDRESSEE: Immunex Corporation, Law Department
;　　STREET: 51 University Street
;　　CITY: Seattle
;　　STATE: WA
;　　COUNTRY: USA
;　　ZIP: 98101
;　COMPUTER READABLE FORM:
;　　MEDIUM TYPE: Floppy disk
;　　COMPUTER: Apple Power Macintosh
;　　OPERATING SYSTEM: Apple Operating System 7.5.5
;　　SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
;　CURRENT APPLICATION DATA:
;　　APPLICATION NUMBER: US/09/215,649A
;　　FILING DATE: 17-Dec-1998
;　　CLASSIFICATION: <Unknown>
;　PRIOR APPLICATION DATA:
;　　APPLICATION NUMBER: 08/996,139
;　　FILING DATE: <Unknown>
;　　APPLICATION NUMBER: USSN 08/813,509
;　　FILING DATE: 07 MARCH 1997
;　　APPLICATION NUMBER: USSN 08/772,330
;　　FILING DATE: 23 DECEMBER 1996
;　ATTORNEY/AGENT INFORMATION:
;　　NAME: Perkins, Patricia Anne
;　　REGISTRATION NUMBER: 34,693
;　　REFERENCE/DOCKET NUMBER: 2851-A
;　TELECOMMUNICATION INFORMATION:
;　　TELEPHONE: (206)587-0430
;　　TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 11:
;　SEQUENCE CHARACTERISTICS:
;　　LENGTH: 294 amino acids
;　　TYPE: amino acid
;　　TOPOLOGY: linear
;　MOLECULE TYPE: protein
;　SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-215-649A-11

Query Match　　　92.8%;　Score 1554;　DB 4;　Length 294;
Best Local Similarity　99.7%;　Pred. No. 2.3e-145;
Matches　293;　Conservative　0;　Mismatches　1;　Indels　0;　Gaps　0;

Qy　23 GVPHEGPLHPAPSAPAPAPPPAASRSMFLALLGLGLGQVVCSIALFLYFRAQMDPNRISE 82
　　　|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　1 GVPHEGPLHPAPSAPAPAPPPAASRSMFLALLGLGLGQVVCSIALFLYFRAQMDPNRISE 60

Qy　83 DSTHCFYRILRLHENAGLQDSTLESEDTLPDSCRRMKQAFQGAVQKELQHIVGPQRFSGA 142
　　　||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　61 DSTHCFYRILRLHENADLQDSTLESEDTLPDSCRRMKQAFQGAVQKELQHIVGPQRFSGA 120

Qy　143 PAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHKVTLSSWYHDRGWAKISNMTLSN 202
　　　||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　121 PAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHKVTLSSWYHDRGWAKISNMTLSN 180

Qy　203 GKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVYVVKTSIKIPSSHNLMKGGSTKN 262
　　　||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　181 GKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMYYVVKTSIKIPSSHNLMKGGSTKN 240

Qy　263 WSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKVQDID 316
　　　|||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　241 WSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKVQDID 294

RESULT 7
US-08-996-139-13
; Sequence 13, Application US/08996139
; Patent No. 6017729
; GENERAL INFORMATION:
;　APPLICANT: Anderson, Dirk M.
;　APPLICANT:　Galibert, Laurent
;　APPLICANT:　Maraskovsky, Eugene
;　TITLE OF INVENTION:　Receptor Activator of NF-kappaB
;　NUMBER OF SEQUENCES: 19
;　CORRESPONDENCE ADDRESS:
;　　ADDRESSEE:　Immunex Corporation, Law Department
;　　STREET:　51 University Street
;　　CITY:　Seattle
;　　STATE:　WA
;　　COUNTRY: USA
;　　ZIP: 98101
;　COMPUTER READABLE FORM:
;　　MEDIUM TYPE:　Floppy disk
;　　COMPUTER:　Apple Power Macintosh
;　　OPERATING SYSTEM:　Apple Operating System 7.5.5
;　　SOFTWARE:　Microsoft Word for Power Macintosh 6.0.1
;　CURRENT APPLICATION DATA:
;　　APPLICATION NUMBER:　US/08/996,139
;　　FILING DATE:　22 DECEMBER 1997
;　　CLASSIFICATION:
;　PRIOR APPLICATION DATA:
;　　APPLICATION NUMBER:　USSN 60/064,671
;　　FILING DATE:　14 OCTOBER 1997
;　PRIOR APPLICATION DATA:
;　　APPLICATION NUMBER:　USSN 08/813,509
;　　FILING DATE:　07 MARCH 1997
;　PRIOR APPLICATION DATA:
;　　APPLICATION NUMBER:　USSN 08/772,330
;　　FILING DATE:　23 DECEMBER 1996
;　ATTORNEY/AGENT INFORMATION:
;　　NAME:　Perkins, Patricia Anne
;　　REGISTRATION NUMBER:　34,693
;　　REFERENCE/DOCKET NUMBER:　2851-A
;　TELECOMMUNICATION INFORMATION:
;　　TELEPHONE:　(206)587-0430
;　　TELEFAX:　(206)233-0644
; INFORMATION FOR SEQ ID NO:　13:
;　SEQUENCE CHARACTERISTICS:
;　　LENGTH:　317 amino acids
;　　TYPE:　amino acid
;　　TOPOLOGY:　linear
;　MOLECULE TYPE:　protein
US-08-996-139-13

Query Match　　　84.6%;　Score 1417.5;　DB 3;　Length 317;
Best Local Similarity　84.3%;　Pred. No. 7.4e-132;
Matches　268;　Conservative　16;　Mismatches　31;　Indels　3;　Gaps　2;

Qy　1 MRRASRDYGKYLRSSEEMGSGPGVPHEGPLHPAPSAPAPAPPPAASRSMFLALLGLGLGQ 60
　　　||||:||| :||||||||| :||||||||||||||||||||||||||||||||||||||||
Db　1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLH-APPPPAPHQPPAASRSMFVALLGLGLGQ 59

Qy　61 VVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESEDT--LPDSCRRM 118
　　　||||:|||||||||||||||||||:|||||||||||||||||:|||||||:||||||||||
Db　60 VVCSVALFFYFRAQMDPNRISEDGTHCIYRLLRLHENADFQDTTLESQDTKLIPDSCRRI 119

Qy　119 KQAFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGS 178
　　　|||||||||||||||||||||||||||||:||| :||||||||:|| ||||||:||||||
Db　120 KQAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGS 179

```
Qy    1  MRRASRDYTKYLRGSEEMGGGPGAPHEGPLH-APPPPAPHQPPAASRSMFVALLGLGLGQ   59
Db   61  VVCSIALFYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESEDT--LPDSCRRM  118
Db   60  VVCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRI 119
Qy  119  KQAFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLTNAASIPSGS  178
Db  120  KQAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTNATDIPSGS  179
Qy  179  HKVTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLM 238
Db  180  HKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLM 239
Qy  239  VYVVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLL 298
Db  240  VYVKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLL  299
Qy  299  DPDQDATYFGAFKVQDID 316
Db  300  DPDQDATYFGAFKVRDID 317
```

```
Qy  179  HKVTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLM 238
Db  180  HKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLM 239
Qy  239  VYVVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLL 298
Db  240  VYVKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLL  299
Qy  299  DPDQDATYFGAFKVQDID 316
Db  300  DPDQDATYFGAFKVRDID 317
```

```
Query Match            84.6%;  Score 1417.5;  DB 4;  Length 317;
Best Local Similarity  84.3%;  Pred. No. 7.4e-132;
Matches  268;  Conservative  16;  Mismatches  31;  Indels  3;  Gaps  2;

Qy    1  MRRASRDYGKYLRSSEEMSGPGVPHEGPLHPAPSAPAPAPPPAASRSMFLALLGLGLGQ   60
```

```
Query Match     84.6%;  Score 1417.5;  DB 4;  Length 317;
Best Local Similarity 84.3%;  Pred. No. 7.4e-132;
Matches  268;  Conservative  16;  Mismatches  31;  Indels  3;  Gaps  2;

Qy    1 MRRASRDYGKYLRSSEEMGSGPGVPHEGPLHPAPSAPAPPPAASRSMFLALLGLGLGQ 60
        ||||||| :|||| |||| | |||||||| || ||       |||||||:||||||||
Db    1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLH-APPPPAPHQPPAASRSMFVALLGLGLGQ 59

Qy   61 VVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESEDT--LPDSCRRM 118
        ||||:|||:||||||||||||||:|||:|||||||||:  |:|:|||:|: : ||||||:
Db   60 VVCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRI 119

Qy  119 KQAFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGS 178
        ||||||||||||||||| |:   |:|  ||||||:| |  ||||||||||||:  ||||
Db  120 KQAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGS 179

Qy  179 HKVTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLM 238
        |||:||||||||||||||||| |||||:||||||||||||||||||||||: :||:|||
Db  180 HKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLM 239

Qy  239 YYVTKTSIKIPSSHNLMKGGSTKNWSGNSEFHYSINVGGFFKLRAGEEISIQVSNPSLL 298
        :||||||||||||||:||||||| ||||||||||||||||||||:||||||:||||||
Db  240 VYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHYSINVGGFFKLRSGEEISIEVSNPSLL 299

Qy  299 DPDQDATYFGAFKVQDID 316
        ||||||||||||| |||
Db  300 DPDQDATYFGAFKVRDID 317

RESULT 10
US-09-052-521C-4
; Sequence 4, Application US/09052521C
; Patent No. 6316408
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; TITLE OF INVENTION: Osteoprotegerin Binding Proteins and Receptors
; FILE REFERENCE: A-451Brv
; CURRENT APPLICATION NUMBER: US/09/052,521C
; CURRENT FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 08/880,855
; PRIOR FILING DATE: 1997-06-23
; PRIOR APPLICATION NUMBER: 08/842,842
; PRIOR FILING DATE: 1997-04-16
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Human
US-09-052-521C-4

Query Match     84.6%;  Score 1417.5;  DB 4;  Length 317;
Best Local Similarity 84.3%;  Pred. No. 7.4e-132;
Matches  268;  Conservative  16;  Mismatches  31;  Indels  3;  Gaps  2;

Qy    1 MRRASRDYGKYLRSSEEMGSGPGVPHEGPLHPAPSAPAPPPAASRSMFLALLGLGLGQ 60
        ||||||| :|||| |||| | |||||||| || ||       |||||||:||||||||
Db    1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLH-APPPPAPHQPPAASRSMFVALLGLGLGQ 59

Qy   61 VVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESEDT--LPDSCRRM 118
        ||||:|||:||||||||||||||:|||:|||||||||:  |:|:|||:|: : ||||||:
Db   60 VVCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRI 119

Qy  119 KQAFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGS 178
        ||||||||||||||||| |:   |:|  ||||||:| |  ||||||||||||:  ||||
Db  120 KQAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGS 179

Qy  179 HKVTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLM 238
        |||:||||||||||||||||| |||||:||||||||||||||||||||||: :||:|||
Db  180 HKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLM 239

Qy  239 YYVTKTSIKIPSSHNLMKGGSTKNWSGNSEFHYSINVGGFFKLRAGEEISIQVSNPSLL 298
        :||||||||||||||:||||||| ||||||||||||||||||||:||||||:||||||
Db  240 VYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHYSINVGGFFKLRSGEEISIEVSNPSLL 299

Qy  299 DPDQDATYFGAFKVQDID 316
        ||||||||||||| |||
Db  300 DPDQDATYFGAFKVRDID 317

RESULT 11
US-09-072-993C-3
; Sequence 3, Application US/09072993C
; Patent No. 6346388
; GENERAL INFORMATION:
; APPLICANT: Michael R. Brigham-Burke
; APPLICANT: Peter R. Young
; TITLE OF INVENTION: A METHOD OF IDENTIFYING AGONIST AND
; TITLE OF INVENTION: ANTAGONISTS FOR TUMOR NECROSIS RELATED RECEPTORS TR1 AND TR2
; FILE REFERENCE: GH-50030
; CURRENT APPLICATION NUMBER: US/09/072,993C
; CURRENT FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/055,513
; PRIOR FILING DATE: 1997-08-13
; PRIOR APPLICATION NUMBER: 60/056,980
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/057,550
; PRIOR FILING DATE: 1997-08-29
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 279
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-072-993C-3

Query Match     15.4%;  Score 258.5;  DB 4;  Length 279;
Best Local Similarity 26.4%;  Pred. No. 1.3e-17;
Matches  78;  Conservative  54;  Mismatches  113;  Indels  51;  Gaps  10;

Qy   43 PAASRSMFLALLGLGLGQVVCSIALFLYFRAQMD--PNRISEDSTHCFYRILRLHENAGL 100
        |: :|  |:||| ::|: | ::  |::||: : :: :||  :|   ||:| ||:||||||
Db    8 PSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACF----LKEDDSY 62

Qy  101 QDSTLESEDTLPDSCRRMKQAFQGAVQK----------ELQHIVGPQRFSGAPAMM 146
        ||  : ::     | :| |:| :|||:           :|: | :|||| |: : :
Db   63 WDP--NDEESMNSPCWQVKWQLRLVRKMILRTSEETISTVQEKQQNISPL--------- 111

Qy  147 EGSWLDVAQRGKPEAQPFAHLT-----INAASIPSGSHKVTL---SSWYHDR-GWAKIS 196
        | | |: :  ||:   :  |::     |: : |: ::|:     :||:|||  ||: ::
Db  112 ------VRERGPQRVA--AHITGTRGRSNTLSSPNSKNEKAIGRKINSWESSRSGHSFLS 163

Qy  197 NMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVYVVKTSIKIPSSHNLMK 256
        | ::|||:| :|:|| | |   ||||::   : :  ::  |: |: | |: ||||::|||
Db  164 NLHLRNGELVIHEKGFYIYSQTYFRFQEEIKENTKNDKQMVQYIYKT-SYPDPILLMK 222

Qy  257 GGSTKNWSGNSEFHYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKV 312
         |     ||: : | |  || |:| : ::||: :    ::|::   |:||||::|
Db  223 SARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 278

RESULT 12
US-08-670-354-2
; Sequence 2, Application US/08670354
; Patent No. 5763223
; GENERAL INFORMATION:
; APPLICANT: Steven R. Wiley and
; APPLICANT: Raymond G. Goodwin.
; TITLE OF INVENTION: Cytokine That Induces Apoptosis
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
```

```
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-584-031-1

Query Match       15.4%;  Score 258.5;  DB 3;  Length 281;
Best Local Similarity  26.4%;  Pred. No. 1.4e-17;
Matches  78;  Conservative  54;  Mismatches 113;  Indels  51;  Gaps  10;

Qy   43  PAASRSMFLALLGLGLGQVVCSIALFLYFRAQMD--PNRISEDSTHCFYRILRLHENAGL 100
             |: .||  :   |:   |   |: :    ::|| ||   ||
Db   10  PSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACF----LKEDDSY 64

Qy  101  QDSTLESEDTLPDSCRRMKQAFQGAVQK-----------------ELQHIVGPQRFSGAPAMM 146
             |  ::: .|  :   |:|
Db   65  WDP--NDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPL---------- 113

Qy  147  EGSWLDVAQRGKPEAQPFAHLT-----INAASIPSGSHKVTL---SSWYHDR-GWAKIS 196
             |:||   ||    :||        ||   :||  : :|
Db  114  ------VRERGPQRVA--AHITGTGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLS 165

Qy  197  NMTLSNGKLRVNQDGFYYLYANICFRHHETSGSSVPTDYLQLMVYVVKTSIKIPSSHNLMK 256
             |: ||:|  ::: ||||:||    |       |      |||
Db  166  NLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYT-SYPDPILLMK 224

Qy  257  GGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKV 312
             | |:|: ||| |||  || ||   :  :|:|||| :
Db  225  SARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 280


RESULT  14
US-08-780-496-1
; Sequence 1, Application US/08780496
; Patent No. 6046048
; GENERAL INFORMATION:
; APPLICANT: Avi Ashkenazi, Anan Chuntharapai, Kyung Jin Kim
; TITLE OF INVENTION: Apo-2 Ligand
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/780,496
; FILING DATE: 08-Jan-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P0978P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5416
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-780-496-1
```

```
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.5.2
; SOFTWARE: Microsoft Word, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/670,354
; FILING DATE: 25-JUN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/496,632
; FILING DATE: 29-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/548,368
; FILING DATE: 01-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Anderson, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2835-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-670-354-2

Query Match       15.4%;  Score 258.5;  DB 1;  Length 281;
Best Local Similarity  26.4%;  Pred. No. 1.4e-17;
Matches  78;  Conservative  54;  Mismatches 113;  Indels  51;  Gaps  10;

Qy   43  PAASRSMFLALLGLGLGQVVCSIALFLYFRAQMD--PNRISEDSTHCFYRILRLHENAGL 100
             |: .||  :   |:   |   |: :    ::|| ||   ||
Db   10  PSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACF----LKEDDSY 64

Qy  101  QDSTLESEDTLPDSCRRMKQAFQGAVQK-----------------ELQHIVGPQRFSGAPAMM 146
             |  ::: .|  :   |:|
Db   65  WDP--NDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPL---------- 113

Qy  147  EGSWLDVAQRGKPEAQPFAHLT-----INAASIPSGSHKVTL---SSWYHDR-GWAKIS 196
             |:||   ||    :||        ||   :||  : :|
Db  114  ------VRERGPQRVA--AHITGTGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLS 165

Qy  197  NMTLSNGKLRVNQDGFYYLYANICFRHHETSGSSVPTDYLQLMVYVVKTSIKIPSSHNLMK 256
             |: ||:|  ::: ||||:||    |       |      |||
Db  166  NLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYT-SYPDPILLMK 224

Qy  257  GGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKV 312
             | |:|: ||| |||  || ||   :  :|:|||| :
Db  225  SARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 280


RESULT  13
US-08-584-031-1
; Sequence 1, Application US/08584031A
; Patent No. 6030945
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: APO-2 LIGAND
; FILE REFERENCE: 11669.22US03
; CURRENT APPLICATION NUMBER: US/08/584,031A
; CURRENT FILING DATE: 1996-01-09
; NUMBER OF SEQ ID NOS: 17
```

Query Match   15.4%;   Score 258.5; DB 3; Length 281;
Best Local Similarity   26.4%; Pred. No. 1.4e-17;
Matches   78; Conservative   54; Mismatches 113; Indels   51; Gaps   10;

Qy   43 PAASRSMFLALLGLGLGQVVCSIALFLYFRAQMD--PNRISEDSTHCFYRILRLHENAGL 100
              |: :: :|| : ||:-:|| || :   :|| :: || ||
Db   10 PSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACF-----LKEDDSY 64

Qy   101 QDSTLESEDTLPDSCRRMKQAFQGAVQK------------ELQHIVGPQRFSGAPAMM 146
              |:|: : : : | : |:|
Db   65 WDP--NDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPL--------- 113

Qy   147 EGSWLDVAQRGKPEAQPFAHLT-----INAASIPSGSHKVTL---SSWYHDR-GWAKIS 196
              : || ||:| || :|| : :   :|| ::
Db   114 ------VRERGPQRVA--AHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLS 165

Qy   197 NMTLSNGKLRVNQDGFYLYANICFRHHETSGSVPTDYLQLMVYVVKTSIKIPSSHNLMK 256
              |:| ||||: ::: |||||::| ::: : | :: : |
Db   166 NLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYT-SYPDPILLMK 224

Qy   257 GGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKV 312
              || || : | :| |:::::::|||||||||
Db   225 SARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 280

RESULT 15
US-08-883-086-10
; Sequence 10, Application US/08883086
; Patent No. 6171787
; GENERAL INFORMATION:
;_ APPLICANT: WILEY, STEVEN
;_ TITLE OF INVENTION: MEMBER OF THE TNF FAMILY USEFUL
;_ TITLE OF INVENTION: FOR TREATMENT AND DIAGNOSIS OF DISEASE
;_ NUMBER OF SEQUENCES: 13
;_ CORRESPONDENCE ADDRESS:
;_   ADDRESSEE: Abbott Laboratories
;_   STREET: 100 Abbott Park Road
;_   CITY: Abbott Park
;_   STATE: IL
;_   COUNTRY: USA
;_   ZIP: 60064-3500
;_ COMPUTER READABLE FORM:
;_   MEDIUM TYPE: Diskette
;_   COMPUTER: IBM Compatible
;_   OPERATING SYSTEM: DOS
;_   SOFTWARE: FastSEQ Version 2.0
;_ CURRENT APPLICATION DATA:
;_   APPLICATION NUMBER: US/08/883,086
;_   FILING DATE:
;_   CLASSIFICATION: 424
;_ PRIOR APPLICATION DATA:
;_   APPLICATION NUMBER:
;_   FILING DATE:
;_ ATTORNEY/AGENT INFORMATION:
;_   NAME: Porembski, Priscilla E.
;_   REGISTRATION NUMBER: 33,207
;_   REFERENCE/DOCKET NUMBER: 6134.US.01
;_ TELECOMMUNICATION INFORMATION:
;_   TELEPHONE: 847-937-0378
;_   TELEFAX: 847-938-2623
;_   TELEX:
; INFORMATION FOR SEQ ID NO: 10:
;_ SEQUENCE CHARACTERISTICS:
;_   LENGTH: 281 amino acids
;_   TYPE: amino acid
;_   STRANDEDNESS: single
;_   TOPOLOGY: linear
;_ MOLECULE TYPE: No. 6171787e
US-08-883-086-10

Query Match   15.4%;   Score 258.5; DB 4; Length 281;
Best Local Similarity   26.4%; Pred. No. 1.4e-17;

Matches   78; Conservative   54; Mismatches 113; Indels   51; Gaps   10;

Qy   43 PAASRSMFLALLGLGLGQVVCSIALFLYFRAQMD--PNRISEDSTHCFYRILRLHENAGL 100
              |: :: :|| : ||:-:|| || :   :|| :: || ||
Db   10 PSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACF-----LKEDDSY 64

Qy   101 QDSTLESEDTLPDSCRRMKQAFQGAVQK------------ELQHIVGPQRFSGAPAMM 146
              |:|: : : : | : |:|
Db   65 WDP--NDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPL--------- 113

Qy   147 EGSWLDVAQRGKPEAQPFAHLT-----INAASIPSGSHKVTL---SSWYHDR-GWAKIS 196
              : || ||:| || :|| : :   :|| ::
Db   114 ------VRERGPQRVA--AHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLS 165

Qy   197 NMTLSNGKLRVNQDGFYLYANICFRHHETSGSVPTDYLQLMVYVVKTSIKIPSSHNLMK 256
              |:| ||||: ::: |||||::| ::: : | :: : |
Db   166 NLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYT-SYPDPILLMK 224

Qy   257 GGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKV 312
              || || : | :| |:::::::|||||||||
Db   225 SARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 280

Search completed: July 15, 2002, 11:01:27
Job time: 22 sec

```
          GenCore version 4.5
      Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on:   July 15, 2002, 11:01:05 ; Search time 30.12 seconds
                                     (without alignments)
                                     1165.316 Million cell updates/sec

Title:         US-09-671-658A-2
Perfect score: 1675
Sequence:      1 MRRASRDYGKYLRSSEEMGS.........LLDPDQDATYFGAFKVQDID 316

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched:      747574 seqs, 11107396 residues

al number of hits satisfying chosen parameters:      747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :  A_Geneseq_032802:*
      1: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:*
      2: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
      3: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1982.DAT:*
      4: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1983.DAT:*
      5: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1984.DAT:*
      6: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1985.DAT:*
      7: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1986.DAT:*
      8: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1987.DAT:*
      9: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1988.DAT:*
     10: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1989.DAT:*
     11: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1990.DAT:*
     12: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1991.DAT:*
     13: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1992.DAT:*
     14: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1993.DAT:*
     15: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1994.DAT:*
     16: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1995.DAT:*
     17: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1996.DAT:*
     18: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1997.DAT:*
     19: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1998.DAT:*
     20: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
     21: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2000.DAT:*
     22: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2001.DAT:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	% Query Match	Query Length	DB	ID	Description
1	1675	100.0	316	19	AAW83194	Human osteoprotege
2	1675	100.0	316	19	AAW83017	Osteoclastogenesis
3	1675	100.0	316	19	AAW59654	Amino acid sequenc
4	1675	100.0	316	20	AAY17874	Murine TRANCE. Mu
5	1675	100.0	316	21	AAY91024	Mouse OBM protein
6	1675	100.0	316	21	AAY84418	Amino acid sequenc
7	1675	100.0	316	21	AAY84419	Rat osteoclast dif
8	1597	95.3	318	22	AAB82092	NF-kB receptor act
9	1554	92.8	294	19	AAW69956	NF-kB receptor act
10	1554	92.8	294	19	AAW68292	Murine receptor ac
11	1554	92.8	294	22	AAE08737	Murine receptor ac
12	1554	92.8	294	22	AAE04425	Murine receptor ac
13	1554	92.8	294	22	AAE01992	Murine RANKL (rece
14	1417.5	84.6	317	19	AAW83195	Human osteoprotege
15	1417.5	84.6	317	19	AAW69957	NF-kB receptor act
16	1417.5	84.6	317	19	AAW68293	NF-kB receptor act
17	1417.5	84.6	317	21	AAY84417	Amino acid sequenc
18	1417.5	84.6	317	22	AAE08738	Human receptor act
19	1417.5	84.6	317	22	AAE04426	Human receptor act
20	1417.5	84.6	317	22	AAE01993	Human full-length
21	1409.5	84.1	317	19	AAW83018	Osteoclastogenesis
22	1318	78.7	501	22	AAB84420	Amino acid sequenc
23	1297	77.4	244	19	AAW83019	A murine OCIF-bind
24	1107	66.1	246	19	AAW83020	Osteoclastogenesis
25	1101	65.7	245	20	AAY17873	Human TRANCE. Hom
26	855	51.0	160	21	AAB08272	Amino acid sequenc
27	852	50.9	173	21	AAY84421	Amino acid sequenc
28	852	50.9	187	21	AAY84420	Amino acid sequenc
29	842	50.3	173	21	AAY84422	A murine osteoprot
30	830	49.6	170	22	AAU08386	Mouse FLAG-murine
31	804.5	48.0	188	21	AAY84423	An osteoprotegerin
32	794.5	47.4	182	21	AAY84424	An osteoprotegerin
33	771	46.0	173	21	AAY84425	DNA encoding osteo
34	768	45.9	160	21	AAB08273	Amino acid sequenc
35	746	44.5	139	21	AAY91023	Mouse OBM protein
36	741	44.2	152	22	AAB67248	Human RANKL. Homo
37	732	43.7	173	21	AAY84426	An osteoprotegerin
38	387	23.1	74	21	AAY91020	Mouse OBM protein
39	285	17.0	54	21	AAY91021	Mouse OBM protein
40	259.5	15.5	281	20	AAY27016	Human Apo-2 ligand
41	259.5	15.5	281	20	AAY27017	Human Apo-2 ligand
42	258.5	15.4	279	19	AAW76332	Human TL2 (TRAIL),
43	258.5	15.4	279	20	AAW95032	Tumour necrosis fa
44	258.5	15.4	281	18	AAW27134	Human Apoptosis in
45	258.5	15.4	281	-18	AAW19787	Human apoptosis in

ALIGNMENTS

```
RESULT  1
AAW83194
ID   AAW83194 standard; Protein; 316 AA.
XX
AC   AAW83194;
XX
DT   11-FEB-1999  (first entry)
XX
DE   Human osteoprotegerin binding protein from the 32D-F3 ins.
XX
KW   Human; osteoprotegerin binding protein; OPG binding protein; arthritis;
KW   osteoporosis; osteoclast maturation; bone disease; metastasis; ODAR;
KW   hypercalcaemia; osteoclast differentiation and activation receptor;
KW   Paget's disease.
XX
OS   Homo sapiens.
XX
PN   WO9846751-A1.
XX
PD   22-OCT-1998.
XX
PF   15-APR-1998;   98WO-US07584.
XX
PR   30-MAR-1998;   98US-0052521.
PR   16-APR-1997;   97US-0842842.
PR   23-JUN-1997;   97US-0880855.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Boyle WJ;
XX
DR   WPI; 1998-594578/50.
DR   N-PSDB; AAV70284.
XX
```

PT   Nucleic acid encoding osteoprotegrin binding protein - useful for,
PT   e.g. treating bone diseases by modulating osteoclast differentiation
PT   and for diagnosis
XX
PS   Claim 19; Fig 1; 47pp; English.
XX
CC   The present sequence is human osteoprotegerin (OPG) binding protein.
CC   Host cells transfected with vectors containing nucleic acid molecules
CC   encoding OPG binding protein are used to produce recombinant OPG binding
CC   protein. OPG binding protein is used in binding assays to determine
CC   osteoprotegrin (OG) in biological samples; to screen for specific
CC   binding agents (particularly agonists and antagonists, including
CC   intracellular proteins); to raise Ab (useful in immunoassays for
CC   detection of OPG binding protein) and to identify compounds that
CC   modulate binding of OPG binding protein to osteoclast differentiation
CC   and activation receptor (ODAR). The nucleic acid molecule encoding OPG
CC   binding protein can be used to detect OPG binding protein-encoding
CC   sequences, e.g. screening for related sequences, also to produce
CC   transgenic animal models, while complementary sequences are used for
CC   antisense regulation of OPG binding protein expression. Modulators of
CC   OPG binding protein, particularly soluble forms of OPG binding protein
CC   or Ab, are used to treat or prevent bone diseases, e.g. osteoporosis,
CC   bone loss caused by arthritis or metastases, hypercalcaemia, Paget's
CC   disease, periodontal disease, osteoporosis, loosening of prostheses,
CC   optionally in combination with agents that promote bone growth.
XX
SQ   Sequence 316 AA;

Query Match   100.0%;   Score 1675;   DB 19;   Length 316;
Best Local Similarity 100.0%; Pred. No. 2.2e-143;
Matches 316;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

Qy   1 MRRASRDYGKYLRSSEEMGSGPGVPHEGPLHPAPSAPAPAPPPAASRMFLALLGLGLGQ 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 mrrasrdygkylrsseemgsgpgvphegplhpapsapapapppaasrmflallglglgq 60

Qy   61 VVCSIALFLYFRAQMDPNRISEDSTHCFYRIRLRHENAGLQDSTLESEDTLPDSCRRMKQ 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 vvcsialflyfraqmdpnrisedsthcfyrirlrhenaglqdstlesedtlpdscrrmkq 120

Qy 121 AFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHK 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 afqgavqkelqhivgpqrfsgapammegswldvaqrgkpeaqpfahltinaasipsgshk 180

Qy 181 VTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYLYANICFRHHETSGSVPTDYLQLMVY 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 vtlsswyhdrgwakisnmtlsngklrvnqdgfyylyanicfrhhetsgsvptdylqlmvy 240

Qy 241 VVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDP 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 vvktsikipsshnlmkggstknwsgnsefhfysinvggffklrageeisiqvsnpslldp 300

Qy 301 DQDATYFGAFKVQDID 316
         ||||||||||||||||
Db 301 dqdatyfgafkvqdid 316

RESULT   2
AAW83017
ID   AAW83017 standard; Protein; 316 AA.
XX
AC   AAW83017;
XX
DT   10-FEB-1999   (first entry)
XX
DE   Osteoclastogenesis inhibitory factor (OCIF)-binding molecule (OBM).
XX
KW   Osteoclastogenesis inhibitory factor; OCIF; OCIF-binding molecule; OBM;
KW   osteoclast; bone absorption factor; bone disorder; calcium metabolism.
XX
OS   Unidentified.
XX

PN   WO9846644-A1.
XX
PD   22-OCT-1998.
XX
PF   15-APR-1998;   98WO-JP01728.
XX
PR   02-DEC-1997;   97JP-0332241.
PR   15-APR-1997;   97JP-0097808.
PR   09-JUN-1997;   97JP-0151434.
PR   12-AUG-1997;   97JP-0217897.
PR   21-AUG-1997;   97JP-0224803.
XX
PA   (SNOW) SNOW BRAND MILK PROD CO LTD.
XX
PI   Goto M, Higashio K, Kinosaki M, Kobayashi F, Morinaga T;
PI   Nakagawa N, Shima N, Takahashi K, Tomoyasu A, Tsuda E;
PI   Washida N, Yamaguchi K, Yano K, Yasuda H;
XX
DR   WPI; 1998-594563/50.
DR   N-PSDB; AAV69886.
XX
PT   Protein binding to osteoclastogenesis inhibitory factor - useful
PT   for, e.g. treatment and investigation of disorders of bone and
PT   calcium metabolism
XX
PS   Claim 8; Pages 106-108; 151pp; Japanese.
XX
CC   The present sequence represents an osteoclastogenesis inhibitory factor
CC   (OCIF)-binding molecule (OBM). The protein promotes and supports the
CC   separation and maturation of osteoclasts in the presence of bone
CC   absorption factors such as calcitriol or parathyroid hormone (PTH).
CC   OBM is isolated from stroma cells cultured in the presence of a bone
CC   absorption factor by separation and solubilisation of membrane proteins
CC   then affinity chromatography using OCIF. It exists in a full-sequence
CC   form and a solubilised form (sOBM) which is a shorter chain. OBM may be
CC   used for screening potential inhibitors and modifiers of its biological
CC   activity, and screening for receptors to OBM which mediate its function.
CC   These substances can then be used in the treatment of disorders of bone
CC   function and calcium metabolism. The antibodies can be used for assay
CC   of the protein, for investigative and diagnostic purposes, and as
CC   components of drugs.
XX
SQ   Sequence 316 AA;

Query Match   100.0%;   Score 1675;   DB 19;   Length 316;
Best Local Similarity 100.0%; Pred. No. 2.2e-143;
Matches 316;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

Qy   1 MRRASRDYGKYLRSSEEMGSGPGVPHEGPLHPAPSAPAPAPPPAASRMFLALLGLGLGQ 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 mrrasrdygkylrsseemgsgpgvphegplhpapsapapapppaasrmflallglglgq 60

Qy   61 VVCSIALFLYFRAQMDPNRISEDSTHCFYRIRLRHENAGLQDSTLESEDTLPDSCRRMKQ 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 vvcsialflyfraqmdpnrisedsthcfyrirlrhenaglqdstlesedtlpdscrrmkq 120

Qy 121 AFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHK 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 afqgavqkelqhivgpqrfsgapammegswldvaqrgkpeaqpfahltinaasipsgshk 180

Qy 181 VTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYLYANICFRHHETSGSVPTDYLQLMVY 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 vtlsswyhdrgwakisnmtlsngklrvnqdgfyylyanicfrhhetsgsvptdylqlmvy 240

Qy 241 VVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDP 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 vvktsikipsshnlmkggstknwsgnsefhfysinvggffklrageeisiqvsnpslldp 300

Qy 301 DQDATYFGAFKVQDID 316
         ||||||||||||||||
Db 301 dqdatyfgafkvqdid 316

```
RESULT  3
AAW59654
ID   AAW59654 standard; Protein; 316 AA.
XX
AC   AAW59654;
XX
DT   24-SEP-1998  (first entry)
XX
DE   Amino acid sequence of mouse 499E9 protein.
XX
KW   Mouse 499E9 protein; polarised Th1 T cell; immune cell; apoptosis;
KW   antagonist; autoimmune disorder; rheumatoid arthritis;
KW   systemic lupus erythematosus; Hashimoto's autoimmune thyroiditis;
KW   acute inflammatory response; antibody; antigen; cancer.
XX
OS   Mus sp.
XX
FH   Key             Location/Qualifiers
FT   Domain          1..49
FT                   /note= "intracellular domain"
FT   Domain          70..316
FT                   /note= "extracellular domain"
XX
PN   WO9825958-A2.
XX
PD   18-JUN-1998.
XX
PF   12-DEC-1997;  97WO-US22766.
XX
PR   13-DEC-1996;  96US-0032846.
XX
PA   (SCHE ) SCHERING CORP.
XX
PI   Gorman DM, Mattson JD;
XX
DR   WPI; 1998-348452/30.
DR   N-PSDB; AAV41489.
XX
PT   Mouse cell surface antigen, 499E9 protein - used to treat conditions
PT   associated with abnormal physiology or development
XX
PS   Claim 1; Pages 8-11; 59pp; English.
XX
CC   This is the amino acid sequence of the mouse 499E9 protein, used
CC   in the method of the invention to treat conditions associated with
CC   abnormal physiology or development. The 499E9 protein is expressed
CC   highly on polarised Th1 T cells, binding of 499E9 to its receptor may
CC   result in either immune cell expansion or apoptosis. Antagonists of
CC   499E9 may be used to modulate immune responses in abnormal situations,
CC   e.g. autoimmune disorders including rheumatoid arthritis, systemic
CC   lupus erythematosus, Hashimoto's autoimmune thyroiditis, as well as
CC   acute inflammatory responses in which T-cell expansion, activation or
CC   immunological T-cell memory play an important role. The antibodies
CC   can be used to raise anti-idiotypic antibodies which will be useful
CC   in detecting or diagnosing various immunological conditions related to
CC   the expression of antigens of 499E9. The antibodies, and fragments of
CC   499E9 can be used in the treatment of conditions associated with
CC   abnormal physiology or development, including abnormal proliferation
CC   (e.g. cancerous conditions) or degenerative conditions.
XX
SQ   Sequence   316 AA;

Query Match             100.0%;   Score 1675;  DB 19;  Length 316;
Best Local Similarity   100.0%;   Pred. NO. 2.2e-143;
Matches  316;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 MRRASRDYGKYLRSSEEMGSGPGVPHEGPLHPAPSAPAPAPPPAASRSMFLALLGLGLGQ 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 mrrasrdygkylrsseemgsgpgvphegplhpapsapapappppaasrsmflallglglgq 60

Qy     61 VVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESEDTLPDSCRRMKQ 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 vvcsialflyfraqmdpnrisedsthcfyrilrlhenaglqdstlesedtlpdscrrmkq 120

Qy    121 AFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHK 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 afqgavqkelqhivgpqrfsgapammegswldvaqrgkpeaqpfahltinaasipsgshk 180

Qy    181 VTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVY 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 vtlsswyhdrgwakisnmtlsngklrvnqdgfyylyanicfrhhetsgsvptdylqlmvy 240

Qy    241 VVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDP 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 vvktsikipsshnlmkggstknwsgnsefhfysinvggffklrageeisiqvsnpslldp 300

Qy    301 DQDATYFGAFKVQDID 316
          |||||||||||||||
Db    301 dqdatyfgafkvqdid 316


RESULT  4
AAY17874
ID   AAY17874 standard; Protein; 316 AA.
XX
AC   AAY17874;
XX
DT   17-AUG-1999  (first entry)
XX
DE   Murine TRANCE.
XX
KW   TRANCE; tumour necrosis factor superfamily; signal transduction; TNF;
KW   TNF-related activation induced cytokine; immune response; cancer;
KW   autoimmune disease; HIV; hypersensitivity; allergen.
XX
OS   Mus musculus.
XX
PN   WO9929865-A2.
XX
PD   17-JUN-1999.
XX
PF   14-DEC-1998;   98WO-US26486.
XX
PR   11-DEC-1998;   98US-0989479.
PR   12-DEC-1997;   97US-0989479.
PR   03-MAR-1998;   98US-0034099.
XX
PA   (UYRQ ) UNIV ROCKEFELLER.
XX
PI   Choi Y, Josien R, Steinman R, Won B;
XX
DR   WPI; 1999-385609/32.
DR   N-PSDB; AAX80224.
XX
PT   TNF like proteins for treating autoimmunity and cancer
XX
PS   Claim 9; Fig 3; 164pp; English.
XX
CC   The present sequence represents murine TNF-related activation induced
CC   cytokines (TRANCE). Human or murine TRANCE polypeptides or their
CC   variants, fragments, derivatives or analogues may be used as modulators
CC   of immune response in a mammal comprising, antisense sequences to
CC   TRANCE and fusion proteins comprising human and/or murine TRANCE.
CC   Agonists and antagonists of TRANCE, can be used to modulate immune
CC   response by increasing or decreasing the life span of mature dendritic
CC   cells and increasing or decreasing T cell activation. These techniques
CC   are especially useful for treating immune system related conditions such
CC   as HIV, cancer, autoimmune disease or hypersensitivity to an allergen.
CC   The TRANCE polypeptides can be used to increase the viability of
CC   dendritic cells in vivo or in vitro, especially when used in conjunction
CC   with proteins of the tumour necrosis factor (TNF) superfamily (especially
CC   CD40L or TNF-alpha).
XX
SQ   Sequence   316 AA;
```

```
Query Match           100.0%;   Score 1675;   DB 20;   Length 316;
Best Local Similarity  100.0%;  Pred. No. 2. 2e-143;
Matches  316;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1 MRRASRDYGKYLRSSEEMGSGPGVPHEGPLHPAPSAPAPAPPPAASRSMFLALLGLGLGQ 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 mrrasrdygkylrsseemgsgpgvphegplhpapsapapapppaasrsmflallglglgq 60

Qy   61 VVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESEDTLPDSCRRMKQ 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 vvcsialflyfraqmdpnrisedsthcfyrilrlhenaglqdstlesedtlpdscrrmkq 120

Qy  121 AFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHK 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 afqgavqkelqhivgpqrfsgapammegswldvaqrgkpeaqpfahltinaasipsgshk 180

Qy  181 VTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYLYANICFRHHETSGSVPTDYLQLMVY 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 vtlsswyhdrgwakisnmtlsngklrvnqdgfyylyanicfrhhetsgsvptdylqlmvy 240

Qy  241 VVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDP 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 vvktsikipsshnlmkggstknwsgnsefhfysinvggffklrageeisiqvsnpslldp 300

Qy  301 DQDATYFGAFKVQDID 316
         |||||||||||||||
Db  301 dqdatyfgafkvqdid 316
```

RESULT 5
AAY91024
ID   AAY91024 standard; Protein; 316 AA.
XX
AC   AAY91024;
XX
DT   05-SEP-2000 (first entry)
XX
DE   Mouse OBM protein sequence SEQ ID NO:10.
XX
KW   Mouse; osteoclastogenesis inhibitory factor binding molecule; OCIF;
KW   OBM; osteoclast; bone absorption promoting factor; vitamin D3; PTH;
KW   parathyroid hormone.
XX
OS   Mus sp.
XX
PN   JP2000102390-A.
XX
PD   11-APR-2000.
XX
PF   30-SEP-1998; 98JP-0292971.
PR   30-SEP-1998; 98JP-0292971.
XX
PA   (SNOW) SNOW BRAND MILK PROD CO LTD.
PA   (YSNE-) YS NEW TECHNOLOGY KENKYUSHO.
XX
DR   WPI; 2000-332087/29.
DR   N-PSDB; AAA39156.
XX
PT   A DNA and preparation of a protein by using it -
XX
PS   Example 1; Page 15-16; 18pp; Japanese.
XX
CC   The present invention describes a genomic DNA encoding a protein having
CC   an activity of supporting or promoting differentiation and maturation of
CC   osteoclasts. The genomic DNA encoding a protein has the following
CC   properties: (a) combines specifically with osteoclastogenesis inhibitory
CC   factor (OCIF) and has a high affinity; (b) shows a molecular weight (mw)
CC   of 30,000 to 40,000 by SDS-PAGE (sodium dodecyl sulfate-polyacrylamide
CC   gel electrophoresis) under a nonreductive condition and the apparent mw
CC   when crosslinked with monomer type OCIF is 90,000 to 110,000; and (c)
CC   has an activity of supporting or promoting differentiation and maturation
CC   of osteoclast in the co-culture of mouse osteoblast-like stroma cell and
CC   mouse spleen cell in the presence of a bone absorption promoting factor
CC   such as active type vitamin D3 and parathyroid hormone (PTH). The protein
CC   can be used as a drug and a research reagent. The present sequence
CC   represents a mouse OCIF binding molecule (OBM) from the present
CC   invention.
XX
SQ   Sequence 316 AA;

```
Query Match           100.0%;   Score 1675;   DB 21;   Length 316;
Best Local Similarity  100.0%;  Pred. No. 2. 2e-143;
Matches  316;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1 MRRASRDYGKYLRSSEEMGSGPGVPHEGPLHPAPSAPAPAPPPAASRSMFLALLGLGLGQ 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 mrrasrdygkylrsseemgsgpgvphegplhpapsapapapppaasrsmflallglglgq 60

Qy   61 VVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESEDTLPDSCRRMKQ 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 vvcsialflyfraqmdpnrisedsthcfyrilrlhenaglqdstlesedtlpdscrrmkq 120

Qy  121 AFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHK 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 afqgavqkelqhivgpqrfsgapammegswldvaqrgkpeaqpfahltinaasipsgshk 180

Qy  181 VTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYLYANICFRHHETSGSVPTDYLQLMVY 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 vtlsswyhdrgwakisnmtlsngklrvnqdgfyylyanicfrhhetsgsvptdylqlmvy 240

Qy  241 VVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDP 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 vvktsikipsshnlmkggstknwsgnsefhfysinvggffklrageeisiqvsnpslldp 300

Qy  301 DQDATYFGAFKVQDID 316
         |||||||||||||||
Db  301 dqdatyfgafkvqdid 316
```

RESULT 6
AAY84418
ID   AAY84418 standard; Protein; 316 AA.
XX
AC   AAY84418;
XX
DT   25-JUL-2000 (first entry)
XX
DE   Amino acid sequence of a murine osteoprotegerin ligand (OPGL).
XX
KW   Osteoprotegerin ligand; OPGL; osteoprotegerin; osteoclastogenesis;
KW   tumour necrosis factor receptor; type II transmembrane protein;
KW   osteoclast differentiation; CSF-1; osteoclast activator;
KW   immune response; osteoporosis; bone resorption.
XX
OS   Mus musculus.
XX
FH   Key   Location/Qualifiers
FT   Domain   48..71
FT   /note= "transmembrane domain"
FT   Domain   70..157
FT   /note= "extracellular stalk domain"
FT   Domain   152..316
FT   /note= "tumour necrosis factor-like domain"
FT   Region   158..317
FT   /note= "active ligand moiety"
XX
PN   WO200015807-A1.
XX
PD   23-MAR-2000.
XX
PF   13-SEP-1999; 99WO-DK00481.
XX

```
KW   tumour necrosis factor receptor; type II transmembrane protein;
KW   osteoclast differentiation; CSF-1; osteoclast activator;|
KW   immune response; osteoporosis; bone resorption.
XX
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
FT   Region          49..69
FT                   /note= "transmembrane region"
FT   Domain          70..157
FT                   /note= "extracellular stalk domain"
FT   Region          158..317
FT                   /note= "active ligand moiety"
XX
PN   WO200015807-A1.
XX
PD   23-MAR-2000.
XX
PF   13-SEP-1999;      99WO-DK00481.
XX
PR   15-SEP-1998;      98DK-0001164.
PR   02-OCT-1998;      98US-0102896.
XX
PA   (MEBI-) M & E BIOTECH AS.
XX
PI   Halkier T, Haaning J;
XX
DR   WPI; 2000-271444/23.
DR   N-PSDB; AZ99966.
XX
PT   In vivo down-regulation of osteoprotegerin ligand (OPGL) activity used
PT   to treat, prevent and ameliorate osteoporosis -
XX
PS   Claim 17; Page 85-86; 110pp; English.
XX
CC   The present sequence represents a murine osteoprotegerin ligand (OPGL).
CC   Osteoprotegerin is a secreted member of the tumour necrosis factor
CC   receptor family, which blocks osteoclastogenesis in a dose dependent
CC   manner. The OPGL protein is synthesised as a type II transmembrane
CC   protein. The murine and human OPGL polypeptides are 87% homologous. OPGL
CC   is a potent osteoclast differentiation factor when combined with CSF-1.
CC   It is not capable of inducing osteoclast differentiation in the absence
CC   of CSF-1. OPGL is also an activator of mature osteoclasts. The
CC   specification describes a method for the in vivo down-regulation of
CC   OPGL activity in an animal. The method comprises using at least one OPGL
CC   polypeptide or subsequence, and/or at least one OPGL analogue to induce
CC   an immune response in the animal. The method and OPGL polypeptide are
CC   useful for treating, preventing and ameliorating osteoporosis or other
CC   diseases or conditions characterised by excessive bone resorption.
XX
SQ   Sequence   316 AA;

Query Match        100.0%;    Score 1675;   DB 21;   Length 316;
Best Local Similarity 100.0%;  Pred. No. 2.2e-143;
Matches 316;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy    1 MRRASRDYGKYLRSSEEMGSGPGVPHEGPLHPAPSAPAPAPPPAASRSMFLALLGLGLGQ 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 mrrasrdygkylrsseemgsgpgvphegplhpapsapapapppaasrsmflallglglgq 60

Qy   61 VVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESEDTLPDSCRRMKQ 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 vvcsialflyfraqmdpnrisedsthcfyrilrlhenaglqdstlesedtlpdscrrmkq 120

Qy  121 AFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHK 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 afqgavqkelqhivgpqrfsgapammegswldvaqrgkpeaqpfahltinaasipsgshk 180

Qy  181 VTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVY 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 vtlsswyhdrgwakisnmtlsngklrvnqdgfyylyanicfrhhetsgsvptdylqlmvy 240
```

```
Qy  241 VVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDP 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 vvktsikipsshnlmkggstknwsgnsefhfysinvggffklrageeisiqvsnpslldp 300

Qy  301 DQDATYFGAFKVQDID 316
          ||||||||||||||||
Db  301 dqdatyfgafkvqdid 316

RESULT  7
AAY84419
ID   AAY84419 standard; Protein; 316 AA.
XX
AC   AAY84419;
XX
DT   25-JUL-2000  (first entry)
XX
DE   Amino acid sequence of a murine osteoprotegerin ligand (OPGL).
XX
KW   Osteoprotegerin ligand; OPGL; osteoprotegerin; osteoclastogenesis;
```

Qy   241 VVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDP 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 vvktsikipsshnlmkggstknwsgnsefhfysinvggffklrageeisiqvsnpslldp 300

Qy   301 DQDATYFGAFKVQDID 316
               |||||||||||||||
Db   301 dqdatyfgafkvqdid 316

RESULT   8
AAB82092
ID   AAB82092 standard; Protein; 318 AA.
XX
AC   AAB82092;
XX
DT   29-JUN-2001 (first entry)
XX
DE   Rat osteoclast differentiation factor, ODF.
XX
KW   Rat; osteoclast formation inducer; vaccine; gene therapy;
KW   Osteoclast Differentiation Factor; bone.
XX
OS   Rattus sp.
XX
PN   WO200123549-A1.
XX
PD   05-APR-2001.
XX
PF   29-SEP-2000; 2000WO-AU01202.
XX
PR   29-SEP-1999; 99AU-0003147.
XX
PA   (UYWA-) UNIV WESTERN AUSTRALIA.
XX
PI   Xu J, Zheng M;
XX
DR   WPI; 2001-335526/35.
DR   N-PSDB; AAF86481.
XX
PT   Novel nucleic acid encoding rat osteoclast differentiation factor
PT   useful for,modulating activity of a cell, e.g., cell proliferation,
PT   cell differentiation and cell viability -
XX
PS   Claim 5; Fig 2; 81pp; English.
XX
CC   The present sequence is the protein sequence for rat Osteoclast
CC   Differentiation Factor (ODF). ODF is thought to be directly involved in
CC   the differentiation of monocytes/macrophages into osteoclasts.
CC   Osteoclasts promote dissolution of the bone matrix and solubilisation of
CC   bone salts. The ODF coding sequence is useful in gene therapy, and as
CC   hybridisation probes or primers. ODF protein is useful for modulating the
CC   activity of cells, e.g., cell proliferation, cell differentiation and
CC   cell viability, as immunogens to generate anti-rat ODF antibodies, and
CC   as vaccines. Anti-rat ODF antibodies are useful in assay methods for
CC   quantifying ODF polypeptides.
XX
SQ   Sequence   318 AA;

Query Match   95.3%; Score 1597; DB 22; Length 318;
Best Local Similarity   95.0%; Pred. No. 2.5e-136;
Matches 302; Conservative 5; Mismatches 9; Indels 2; Gaps 1;

Qy   1 MRRASRDYGKYLRSSEEMGSGPGVPHEGPLHPAPSAPAPAPPPAASRMFLALLGLGLGQ 60
              ||||:||||||| |||||| ||||||||||||||||||||||| ||||||||||||
Db   1 mrranrdygkylrgseemgscpgvpheplhpapsapapppaasrmflallglglgq 60

Qy   61 VVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESEDT--LPDSCRRM 118
              ||||||||||||| ||||||||:| || ||||||||| | ||||||||| |||||||||
Db   61 vvcsialflyfraqmdpnrisedstrcfyrilrlrentglqdstlesedtealpdscrrm 120

Qy   119 KQAFGGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGS 178
              |||||||||||||||||||::|||||||||||||||| |||||||||||||||||| ||||||

```
CC   nucleic acid can be used to produce recombinant RANK protein. The soluble
CC   RANK may be used for inhibiting activation of NF-kB, by contacting a cell
CC   expressing membrane-associated RANK with a soluble RANK which binds to
CC   RANK ligand (RANKL). The soluble RANK polypeptide composition may also be
CC   used for regulating an immune or inflammatory response. Inhibition of
CC   NF-kB by RANK antagonists may be useful in ameliorating negative effects
CC   of an inflammatory response that result from triggering of RANK, e.g. in
CC   treating toxic shock or sepsis, graft-versus-host reactions, or acute
CC   inflammatory reactions. They can also be used in adjunct therapy for
CC   disease characterised by neoplastic cells that express RANK. The products
CC   can also be used for detection and drug screening.
XX
SQ   Sequence   294 AA;

Query Match            92.8%;  Score 1554;  DB 19;  Length 294;
Best Local Similarity  99.7%;  Pred. No. 1.8e-132;
Matches  293;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy   23 GVPHEGPLHPAPSAPAPAPPPAASRSMFLALLGLGLGQVVCSIALFLYFRAQMDPNRISE 82
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 gvphegplhpapsapapapppaasrsmflallglglgqvvcsialflyfraqmdpnrise 60

Qy   83 DSTHCFYRILRLHENAGLQDSTLESEDTLPDSCRRMKQAFQGAVQKELQHIVGPQRFSGA 142
         ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db   61 dsthcfyrilrlhenadiqdstlesedtlpdscrrmkqafqgavqkelqhivgpqrfsga 120

Qy  143 PAMMEGSWLDVAQRGKPEAQFAHLTINAASIPSGSHKVTLSSWYHDRGWAKISNMTLSN 202
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 pammegswldvaqrgkpeaqfahltinaasipsgshkvtlsswyhdrgwakisnmtlsn 180

Qy  203 GKLRVNQDGFYYLYANICFRHHETSGSSVPTDYLQLMVYVVKTSIKIPSSHNLMKGGSTKN 262
         ||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db  181 gklrvnqddgfyylyanicfrhhetsgsvptdylqlmvyvvktsikipsshnlmkggstkn 240

Qy  263 WSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKVQDID 316
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 wsgnsefhfysinvggffklrageeisiqvsnpslldpdqdatyfgafkvqdid 294

RESULT 11
AAE08737
ID   AAE08737 standard; Protein; 294 AA.
XX
AC   AAE08737;
XX
DT   15-NOV-2001   (first entry)
XX
DE   Murine receptor activator of NF kappaB ligand (RANKL) protein.
XX
KW   Murine; receptor activator of nuclear factor kappaB ligand; RANKL; NF;
KW   tumour necrosis factor; TNF; TNF receptor associated factor; TRAF;
KW   immune response; inflammatory response; graft-versus-host reaction;
KW   toxic shock; sepsis; acute inflammatory reaction; bone resorption;
KW   anti-apoptotic signal; therapy; immunosuppressant; anti-inflammatory.
XX
OS   Mus musculus.
XX
PN   US6271349-B1.
XX
PD   07-AUG-2001.
XX
PF   17-DEC-1998;   98US-0215649.
XX
PR   23-DEC-1996;   96US-0059978.
PR   07-MAR-1997;   97US-0077181.
PR   14-OCT-1997;   97US-0064671.
PR   23-DEC-1996;   96US-0772330.
PR   07-MAR-1997;   97US-0813509.
PR   22-DEC-1997;   97US-0996139.
XX
PA   (IMMV ) IMMUNEX CORP.
XX
```

```
CC   screening.
XX
SQ   Sequence   294 AA;

Query Match            92.8%;  Score 1554;  DB 19;  Length 294;
Best Local Similarity  99.7%;  Pred. No. 1.8e-132;
Matches  293;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy   23 GVPHEGPLHPAPSAPAPAPPPAASRSMFLALLGLGLGQVVCSIALFLYFRAQMDPNRISE 82
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 gvphegplhpapsapapapppaasrsmflallglglgqvvcsialflyfraqmdpnrise 60

Qy   83 DSTHCFYRILRLHENAGLQDSTLESEDTLPDSCRRMKQAFQGAVQKELQHIVGPQRFSGA 142
         ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db   61 dsthcfyrilrlhenadiqdstlesedtlpdscrrmkqafqgavqkelqhivgpqrfsga 120

Qy  143 PAMMEGSWLDVAQRGKPEAQFAHLTINAASIPSGSHKVTLSSWYHDRGWAKISNMTLSN 202
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 pammegswldvaqrgkpeaqfahltinaasipsgshkvtlsswyhdrgwakisnmtlsn 180

Qy  203 GKLRVNQDGFYYLYANICFRHHETSGSSVPTDYLQLMVYVVKTSIKIPSSHNLMKGGSTKN 262
         ||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db  181 gklrvnqddgfyylyanicfrhhetsgsvptdylqlmvyvvktsikipsshnlmkggstkn 240

Qy  263 WSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKVQDID 316
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 wsgnsefhfysinvggffklrageeisiqvsnpslldpdqdatyfgafkvqdid 294

RESULT 10
AAW68292
ID   AAW68292 standard; Protein; 294 AA.
XX
AC   AAW68292;
XX
DT   08-OCT-1998   (first entry)
XX
DE   NF-kB receptor activator RANK ligand (RANKL).
XX
KW   RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;
KW   immune response; inflammatory response; toxic shock; sepsis;
KW   RANKL; RANK ligand; tumour necrosis factor; TNF; mouse.
XX
OS   Mus musculus.
XX
XX
PN   WO9828424-A2.
XX
PD   02-JUL-1998.
XX
PF   22-DEC-1997;   97WO-US23866.
XX
PR   14-OCT-1997;   97US-0064671.
PR   23-DEC-1996;   96US-0059978.
PR   07-MAR-1997;   97US-0813509.
XX
PA   (IMMV ) IMMUNEX CORP.
XX
PI   Anderson DM, Galibert LJ, Maraskovsky E;
XX
DR   WPI; 1998-377655/32.
DR   N-PSDB; AAV41371.
XX
PT   New isolated receptor activator of necrosis factor-kappa B - useful
PT   for, e.g. developing products for regulating an immune or
PT   inflammatory response, treating toxic shock or sepsis
XX
PS   Example 7; Pages 55-57; 80pp; English.
XX
CC   This represents a murine RANKL, a ligand for the RANK (receptor
CC   activator of necrosis factor-kappaB (NF-kB)) polypeptide. RANK is a
CC   member of the tumour necrosis factor (TNF) family. Host cells transformed
CC   or transfected with an expression vector comprising the RANK encoding
```

PI   Dougall WC, Galibert L;
XX
DR   WPI; 2001-520313/57.
DR   N-PSDB; AAD15310.
XX
PT   New receptor activator of NF-kappaB (RANK) polypeptides, useful for
PT   regulating immune response, in screening for RANK inhibitors, or as an
PT   adjunct therapy for disease characterized by neoplastic cells that
PT   express RANK -
XX
PS   Example 15; Column 65-68; 47pp; English.
XX
CC   The patent discloses novel receptor activator of nuclear factor (NF)-
CC   kappaB (RANK) proteins and their corresponding DNAs. RANK is a member
CC   of the tumour necrosis factor (TNF) receptor superfamily and associates
CC   with TNF receptor associated factor (TRAF) 2 and 3 which are important
CC   in the regulation of immune and inflammatory response. The receptors
CC   are useful for regulating immune response and in screening for inhibitors
CC   of these receptors. The cytoplasmic domain of RANK is used in developing
CC   assays for inhibitors of signal transduction, e.g. for screening for
CC   molecules that inhibit interaction of RANK with TRAF1, TRAF2, TRAF3,
CC   TRAF5 and particularly TRAF6. NF-kappaB inhibition by RANK antagonists
CC   are useful in ameliorating the negative effects of an inflammatory
CC   response that result from triggering of RANK, e.g. in treating toxic
CC   shock or sepsis, graft-versus-host reactions, acute inflammatory
CC   reactions and the effects of bone resorption. RANK acts as an anti-
CC   apoptotic signal and rescue the cells that express RANK from apoptosis.
CC   Soluble forms of the receptor are used in vivo or in vitro based
CC   screening tests for agonists or antagonists of RANK activity, as
CC   antagonists of RANK-mediated NF-kappa B activation, or to inhibit
CC   transduction of a signal via RANK. RANK compositions are used in the
CC   development of both agonistic and antagonistic antibodies, or as an
CC   adjunct therapy for disease characterised by neoplastic cells that
CC   express RANK. Compounds that interfere with RANK/TRAF6 interactions
CC   are useful for modulating the formation of osteoclasts from osteoclast
CC   precursors and for modulating osteoclast function and activities. They
CC   are used as inhibitors of diseases associated with excess bone resorption
CC   and as immunosuppressants or anti-inflammatory agents. The RANK DNAs are
CC   useful for the expression of recombinant proteins, as probes for analysis
CC   of the presence or distribution of RANK transcripts, while the proteins
CC   are useful in preparing kits for the detection of soluble RANK, or
CC   monitor RANK-related activity. The present sequence is RANK ligand
CC   (RANKL) protein from murine.
XX
SQ   Sequence   294 AA;

Query Match   92.8%;   Score 1554; DB 22;   Length 294;
Best Local Similarity 99.7%;   Pred. No. 1.8e-132;
Matches 293;   Conservative 0;   Mismatches 0;   Indels   1;   Gaps   0;

Qy   23 GVPHEGPLHPAPSAPAPAPPPAASRSMFLALLGLGLGQVVCSIALFLYFRAQMDPNRISE 82
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 gvphegplhpapsapapapppaasrsmflallglglgqvvcsialflyfraqmdpnrise 60

Qy   83 DSTHCFYRILRLHENAGLQDSTLESEDTLPDSCRRMKQAFQGAVQKELQHIVGPQRFSGA 142
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 dsthcfyrilrlhenadlqdstlesedtlpdscrrmkqafqgavqkelqhivgpqrfsga 120

Qy   143 PAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHKVTLSSWYHDRGWAKISNMTLSN 202
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 pammegswldvaqrgkpeaqpfahltinaasipsgshkvtlsswyhdrgwakisnmtlsn 180

Qy   203 GKLRVNQDGFYLYANICFRHHETSGSVPTDYLQLMVYVVKTSIKIPSSHNLMKGGSTKN 262
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 gklrvnqdgfyylyanicfrhhetsgsvptdylqlmvyvvktsikipsshnlmkggstkn 240

Qy   263 WSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDDQDATYFGAFKVQDID 316
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 wsgnsefhfysinvggffklrageeisiqvsnpslldpdqddatyfgafkvqdid 294

RESULT 12

AAE04425
ID   AAE04425 standard; Protein; 294 AA.
XX
AC   AAE04425;
XX
DT   04-SEP-2001 (first entry)
XX
DE   Murine receptor activator of NF-chi B ligand (RANKL) protein.
XX
KW   Murine; receptor activator of NF-chi B; RANK; tumour necrosis factor;
KW   CD40; TNF receptor-associated factor; TRAF; ligand; immune response; TNF;
KW   chromosome 18q22.1; RANKL; chromosome 13q14; transmembrane protein.
XX
OS   Mus musculus.
XX
FH   Location/Qualifiers
FT   Region   139..294
FT   /note="Receptor binding region"
XX
PN   US6242213-B1.
XX
PD   05-JUN-2001.
XX
PF   22-DEC-1997;   97US-0995659.
XX
PR   23-DEC-1996;   96US-0059978.
PR   07-MAR-1997;   97US-077181.
PR   14-OCT-1997;   97US-0064671.
XX
PA   (IMMV) IMMUNEX CORP.
XX
PI   Anderson DM;
XX
DR   WPI; 2001-407216/43.
DR   N-PSDB; AAD08714.
XX
PT   New DNA molecules, useful for producing ligands (which are useful for
PT   regulating immune response and in screening for inhibitors of NF-chi B
PT   receptor activator) of the receptor activator of NF-chi B (RANK) -
XX
PS   Example 7; Column 59-62; 43pp; English.
XX
CC   The present invention relates to receptor activator of NF-chi B (RANK)
CC   DNA. RANK is mapped to chromosome 18q22.1 and its ligand (RANKL) to
CC   chromosome 13q14. RANK and RANKL are type 1 and type 2 transmembrane
CC   proteins respectively. RANK is a member of the tumour necrosis factor
CC   (TNF) superfamily and it closely resembles CD40 in the extracellular
CC   region. RANK associates with TNF receptor-associated factor (TRAF) 2
CC   and TRAF3. The DNA molecules are useful for producing ligands of RANK.
CC   The ligands are useful for regulating immune response and in screening
CC   for inhibitors of RANK. The present sequence is murine RANKL protein.
XX
SQ   Sequence   294 AA;

Query Match   92.8%;   Score 1554; DB 22;   Length 294;
Best Local Similarity 99.7%;   Pred. No. 1.8e-132;
Matches 293;   Conservative 0;   Mismatches 0;   Indels   1;   Gaps   0;

Qy   23 GVPHEGPLHPAPSAPAPAPPPAASRSMFLALLGLGLGQVVCSIALFLYFRAQMDPNRISE 82
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 gvphegplhpapsapapapppaasrsmflallglglgqvvcsialflyfraqmdpnrise 60

Qy   83 DSTHCFYRILRLHENAGLQDSTLESEDTLPDSCRRMKQAFQGAVQKELQHIVGPQRFSGA 142
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 dsthcfyrilrlhenadlqdstlesedtlpdscrrmkqafgqavqkelqhivgpqrfsga 120

Qy   143 PAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHKVTLSSWYHDRGWAKISNMTLSN 202
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 pammegswldvaqrgkpeaqpfahltinaasipsgshkvtlsswyhdrgwakisnmtlsn 180

Qy   203 GKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVYVVKTSIKIPSSHNLMKGGSTKN 262
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

```
Qy     23  GVPHEGPLHPAPSAPAPAPPPAASRMFLALLGLGLGQVVCSIALFLYFRAQMDPNRISE 82
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1  gvphegplhpapsapapapppaasrmflallglglgqvvcsialflyfraqmdpnrise 60

Qy     83  DSTHCFYRILRHENAGLQDSTLESEDTLPDSCRRMKQAFOGAVQKELQHIVGPQRFSGA 142
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61  dsthcfyrilrhenadlqdstlesedtlpdscrrmkqafggavqkelqhivgpqrfsga 120

Qy    143  PAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHKVTLSSWYHDRGWAKISNMTLSN 202
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121  pammegswldvaqrgkpeaqpfahltinaasipsgshkvtlsswyhdrgwakisnmtlsn 180

Qy    203  GKLRVNQDGFYYLYANICFRHETSGSVPTDYLQLMVYVVKTSIKIPSSHNLMKGGSTKN 262
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181  gklrvnqdgfyylyanicfrhetsgsvptdylqlmvyvvktsikipsshnlmkggstkn 240

Qy    263  WSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKVQDID 316
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241  wsgnsefhfysinvggffklrageeisiqvsnpslldpdqdatyfgafkvqdid 294
```

RESULT 13
AAE01992
ID   AAE01992 standard; Protein; 294 AA.
XX
AC   AAE01992;
XX
DT   31-JUL-2001 (first entry)
XX
DE   Murine RANKL (receptor activator of NF-kappaB ligand) protein.
XX
KW   Mouse; receptor activator of NF-kappaB; RANK; nuclear factor-kappaB;
KW   NF-kappaB; tumour necrosis factor; TNF; type I transmembrane protein;
KW   TNF receptor-associated factor; TRAF; RANK ligand; RANKL; osteopathic;
KW   inflammatory reaction; bone resorption; gene therapy; immunomodulator;
KW   immune system dysfunction; familial expansile osteolysis; FEO;
KW   early onset Paget's disease of bone; EP; cytostatic.
XX
OS   Mus musculus.
XX
PN   WO200136637-A1.
XX
PD   25-MAY-2001.
XX
PF   14-NOV-2000; 2000WO-US31459.
XX
PR   17-NOV-1999; 99US-0442029.
XX
PA   (IMMV) IMMUNEX CORP.
XX
PI   Anderson DM, Hughes AE;
XX
DR   WPI; 2001-329222/34.
DR   N-PSDB; AAD05903.
XX
PT   New DNA encoding a receptor activator of NF-kappaB polypeptide for the
PT   treatment of Paget's disease and Familial Expansile Osteolysis (FEO) -
XX
PS   Disclosure; Page 74-75; 96pp; English.
XX
CC   The present invention relates to a novel receptor, referred to as RANK
CC   (receptor activator of NF (nuclear factor)-kappaB), a member of TNF
CC   (tumour necrosis factor) receptor superfamily. RANK is a Type I
CC   transmembrane protein that interacts with TNF receptor-associated
CC   factors (TRAFs). Triggering of RANK by overexpression or co-expression
CC   of RANK and membrane bound RANK ligand (RANKL) results in upregulation
CC   of the transcription factor NF-kappaB, a ubiquitous transcription factor
CC   that is most extensively utilised in cells of the immune system.
CC   Inhibition of NF-kappaB by RANK antagonists is useful in ameliorating
CC   negative effects of inflammatory reactions, and the effects of excess
CC   bone resorption. The RANK DNAs, proteins and their analogues are useful
CC   for the preparation of pharmaceutical compositions, for infecting target
CC   cells for use in gene therapy applications in diagnosing diseases
CC   associated with RANK, and as targets for use in screening assays. They
CC   may be used in the treatment or diagnosis of immune system dysfunction.
CC   The present invention also encompasses gene therapy methods to correct
CC   gene-activating mutations, associated with e.g. familial expansile
CC   osteolysis (FEO) and early onset Paget's disease of bone (EP). The
CC   present amino acid sequence is murine RANKL (muRANKL) protein.
XX
SQ   Sequence   294 AA;

Query Match   92.8%;   Score 1554; DB 22; Length 294;
Best Local Similarity 99.7%;   Pred. No. 1.8e-132;
Matches 293;   Conservative   0;   Mismatches   1;   Indels   0;   Gaps   0;

```
Db    181  gklrvnqdgfyylyanicfrhetsgsvptdylqlmvyvvktsikipsshnlmkggstkn 240

Qy    263  WSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKVQDID 316
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241  wsgnsefhfysinvggffklrageeisiqvsnpslldpdqdatyfgafkvqdid 294
```

RESULT 14
AAW83195
ID   AAW83195 standard; Protein; 317 AA.
XX
AC   AAW83195;
XX
DT   11-FEB-1999 (first entry)
XX
DE   Human osteoprotegerin binding protein from the pcDNA/huOPGbp1.1insert.
XX
KW   Human; osteoprotegerin binding protein; OPG binding protein; arthritis;
KW   osteoporosis; osteoclast maturation; bone disease; metastasis; ODAR;
KW   hypercalcaemia; osteoclast differentiation and activation receptor;
KW   Paget's disease.
XX
OS   Homo sapiens.
XX
PN   WO9846751-A1.
XX
PD   22-OCT-1998.
XX
PF   15-APR-1998;   98WO-US07584.
XX
PR   30-MAR-1998;   98US-0052521.
PR   16-APR-1997;   97US-0842842.
PR   23-JUN-1997;   97US-0880855.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Boyle WJ;
XX
DR   WPI; 1998-594578/50.
DR   N-PSDB; AAV70285.
XX
PT   Nucleic acid encoding osteoprotegrin binding protein - useful for;
PT   e.g. treating bone diseases by modulating osteoclast differentiation
PT   and for diagnosis
XX
PS   Claim 19; Fig 4; 47pp; English.
XX
CC   The present sequence is human osteoprotegerin (OPG) binding protein.
CC   Host cells transfected with vectors containing nucleic acid molecules
CC   encoding OPG binding protein are used to produce recombinant OPG binding
CC   protein. OPG binding protein is used in binding assays to determine
CC   osteoprotegrin (OG) in biological samples; to screen for specific
CC   binding agents (particularly agonists and antagonists, including
CC   intracellular proteins); to raise Ab (useful in immunoassays for
CC   detection of OPG binding protein) and to identify compounds that
CC   modulate binding of OPG binding protein to osteoclast differentiation
CC   and activation receptor (ODAR). The nucleic acid molecule encoding OPG
CC   binding protein can be used to detect OPG binding protein-encoding
CC   sequences, e.g. screening for related sequences, also to produce
```

PT  New isolated ligand for receptor activator of NF-kappa B - used to
PT  develop products for augmenting an immune response for inhibiting an
PT  inflammatory response and for protection of cells
XX
PS  Claim 27; Pages 59-60; 80pp; English.
XX
CC  This represents a human RANKL, a ligand for the RANK (receptor
CC  activator of necrosis factor-kappaB (NF-kB) polypeptide. RANK is a
CC  member of the tumour necrosis factor (TNF) family. A soluble RANK
CC  may be used for inhibiting activation of NF-kB, by contacting a cell
CC  expressing membrane-associated RANK with a soluble RANK which binds to
CC  RANK ligand (RANKL). RANKL polypeptides can activate RANK and can be
CC  used to induce maturation of dendritic cells and enhance their
CC  allo-stimulatory capacity, thereby augmenting an immune response. The
CC  soluble RANK polypeptide composition may also be used for regulating an
CC  immune or inflammatory response. Inhibition of NF-kB by RANK antagonists
CC  may be useful in ameliorating negative effects of an inflammatory
CC  response that result from triggering of RANK, e.g. in treating toxic
CC  shock or sepsis, graft-versus-host reactions, or acute inflammatory
CC  reactions. They can also be used in adjunct therapy for disease
CC  characterised by neoplastic cells that express RANK. RANKL polypeptides
CC  can also be used to identify inhibitors of RANK and thus inhibitors of
CC  an inflammatory response, and also for protecting RANK-expressing cells
CC  from the negative effects of chemotherapy or the presence of high levels
CC  of TNF-alpha. The products can also be used for detection and drug
CC  screening.
XX
SQ  Sequence   317 AA;

Query Match              84.6%;  Score 1417.5;  DB 19;  Length 317;
Best Local Similarity    84.3%;  Pred. No. 4.4e-120;
Matches  268;  Conservative  16;  Mismatches  31;  Indels  3;  Gaps  2;

Qy    1 MRRASRDYGKYLRSSEEMGSGPGVPHEGPLHPAPSAPAPAPPPAASRSMFLALLGLGLGQ 60
         |||||||| |||| ||||||| ||||||||||||| ||||||||||||||||||||||
Db    1 mrrasrdytkylrgseemgsgpggpgaphegplh-appppahqppaasrsmfvallglglgq 59

Qy   61 VVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESEDT--LPDSCRRM 118
         |||:||| |||||||||||||||| || |||||||| |||:||| :||||: :|||||:
Db   60 vvcsvlffyfraqmdpnrisedgthclyrilrlhenadfqdttlesqdtklipdscrri 119

Qy  119 KQAFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGS 178
         ||||||||||||||| | ::|||||:| | ||||||| |||||
Db  120 kqafqgavqkelqhivgsqhiraekanvdgswldlakrskleaqpfahltinatdipsgs 179

Qy  179 HKVTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLM 238
         |||:|||||||||||||| ||||||:| |||| ||||||||:|| :|||||||||||||
Db  180 hkvslsswyhdrgwakisnmtfsngklivnqdgfyylyanicfrhhetsgdlateylqlm 239

Qy  239 VYVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLL 298
         ||| ||||||||| ||||||::|||||||||||||||||||||||:||||||||||||
Db  240 vyvtktsikipsshtlmkggstkywsgnsefhfysinvggffkirsgeeislevsnpsll 299

Qy  299 DPDQDATYFGAFKVQDID 316
         |||||||||||||:|||
Db  300 dpdqdatyfgafkvrdid 317

Search completed: July 15, 2002, 11:02:28
Job time: 83 sec

---

CC  transgenic animal models, while complementary sequences are used for
CC  antisense regulation of OPG binding protein expression. Modulators of
CC  OPG binding protein, particularly soluble forms of OPG binding protein
CC  or Ab, are used to treat or prevent bone diseases, e.g. osteoporosis,
CC  bone loss caused by arthritis or metastases, hypercalcaemia, Paget's
CC  disease, periodontal disease, osteoporosis, loosening of prostheses,
CC  optionally in combination with agents that promote bone growth.
XX
SQ  Sequence   317 AA;

Query Match              84.6%;  Score 1417.5;  DB 19;  Length 317;
Best Local Similarity    84.3%;  Pred. No. 4.4e-120;
Matches  268;  Conservative  16;  Mismatches  31;  Indels  3;  Gaps  2;

Qy    1 MRRASRDYGKYLRSSEEMGSGPGVPHEGPLHPAPSAPAPAPPPAASRSMFLALLGLGLGQ 60
         |||||||| |||| ||||||| ||||||||||||| ||||||||||||||||||||||
Db    1 mrrasrdytkylrgseemgsgpggpgaphegplh-appppahqppaasrsmfvallglglgq 59

Qy   61 VVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESEDT--LPDSCRRM 118
         |||:||| |||||||||||||||| || |||||||| |||:||| :||||: :|||||:
Db   60 vvcsvlffyfraqmdpnrisedgthclyrilrlhenadfqdttlesqdtklipdscrri 119

Qy  119 KQAFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGS 178
         ||||||||||||||| | ::|||||:| | ||||||| |||||
Db  120 kqafqgavqkelqhivgsqhiraekanvdgswldlakrskleaqpfahltinatdipsgs 179

Qy  179 HKVTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLM 238
         |||:|||||||||||||| ||||||:| |||| ||||||||:|| :|||||||||||||
Db  180 hkvslsswyhdrgwakisnmtfsngklivnqdgfyylyanicfrhhetsgdlateylqlm 239

Qy  239 VYVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLL 298
         ||| ||||||||| ||||||::|||||||||||||||||||||||:||||||||||||
Db  240 vyvtktsikipsshtlmkggstkywsgnsefhfysinvggffkirsgeeislevsnpsll 299

Qy  299 DPDQDATYFGAFKVQDID 316
         |||||||||||||:|||
Db  300 dpdqdatyfgafkvrdid 317

RESULT 15
AAW69957
ID   AAW69957 standard; Protein; 317 AA.
XX
AC   AAW69957;
XX
DT   08-OCT-1998 (first entry)
XX
DE   NF-kB receptor activator RANK ligand (RANKL).
XX
KW   RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;
KW   immune response; inflammatory response; toxic shock; sepsis;
KW   RANKL; RANK ligand; tumour necrosis factor; TNF.
XX
OS   Homo sapiens.
XX
PN   WO9828426-A2.
XX
PD   02-JUL-1998.
XX
PF   22-DEC-1997; 97WO-US23775.
XX
PR   14-OCT-1997; 97US-0064671.
PR   23-DEC-1996; 96US-0059978.
PR   07-MAR-1997; 97US-0813509.
XX
PA   (IMMV ) IMMUNEX CORP.
XX
PI   Anderson DM, Galibert LJ, Maraskovsky E;
XX
DR   WPI; 1998-377657/32.
DR   N-PSDB; AAV41378.
XX

```
                    GenCore version 4.5
          Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on:     July 15, 2002, 11:01:30 ; Search time 30.24 Seconds
                                        (without alignments)
                                        1807.751 Million cell updates/sec

Title:      US-09-671-658A-2
Perfect score:   1675
Sequence:   1 MRRASRDYGKYLRSSEEMGS.........LLDPDQDATYFGAFKVQDID  316

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:   562222 seqs, 172994929 residues

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :  SPTREMBL_19:*
        1:  sp_archea:*
        2:  sp_bacteria:*
        3:  sp_fungi:*
        4:  sp_human:*
        5:  sp_invertebrate:*
        6:  sp_mammal:*
        7:  sp_mhc:*
        8:  sp_organelle:*
        9:  sp_phage:*
       10:  sp_plant:*
       11:  sp_rodent:*
       12:  sp_virus:*
       13:  sp_vertebrate:*
       14:  sp_unclassified:*
       15:  sp_rvirus:*
       16:  sp_bacteriap:*
       17:  sp_archeap:*

Total number of hits satisfying chosen parameters:        562222
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1646.5	98.3	313	11	Q9R1Y0	Q9r1y0 mus musculu
2	1597	95.3	318	11	Q9ESE2	Q9ese2 rattus norv
3	1476.5	88.1	287	11	Q9JJK9	Q9jjk9 mus musculu
4	1220	72.8	270	4	Q96Q17	Q96q17 homo sapien
5	1057	63.1	199	11	Q9JJK8	Q9jjk8 mus musculu
6	272	16.2	53	11	Q9IZI9	Q9izi9 rattus norv
7	263.5	15.7	214	13	Q9DDZ5	Q9ddz5 brachydanio
8	217.5	13.0	287	13	Q90WT9	Q90wt9 gallus gall
9	188.5	11.3	261	6	Q9BDN3	Q9bdn3 callithrix
10	182.5	10.9	261	6	Q9BDM3	Q9bdm3 aotus trivi
11	179.5	10.7	282	6	Q9BEA8	Q9bea8 sus scrofa
12	179.5	10.7	282	6	Q95M04	Q95m04 sus scrofa
13	179	10.7	280	6	Q9BDM5	Q9bdm5 macaca mula
14	178.5	10.7	282	6	Q95N10	Q95n10 sus scrofa
15	178	10.6	280	6	Q9MYL6	Q9myl6 macaca neme
16	177	10.6	280	6	Q9BDN1	Q9bdn1 cercocebus
17	176.5	10.5	261	6	Q9BDC7	Q9bdc7 macaca mula
18	168.5	10.1	272	13	Q9I8D8	Q9i8d8 gallus gall
19	151	9.0	240	6	Q9BDM7	Q9bdm7 macaca neme
20	149	8.9	234	6	Q9TTJ3	Q9ttj3 equus cabal
21	148	8.8	232	11	O35853	O35853 mus musculu
22	147.5	8.8	310	11	Q9JM10	Q9jm10 marmota mon
23	146.5	8.7	239	11	Q9QYH9	Q9qyh9 mus musculu
24	145	8.7	260	11	Q922V2	Q922v2 rattus norv
25	145	8.7	260	11	Q9R254	Q9r254 rattus norv
26	142	8.5	232	4	Q9UIV3	Q9uiv3 homo sapien
27	140.5	8.4	310	11	Q9JM11	Q9jm11 marmota mon
28	140	8.4	174	4	O95150	O95150 homo sapien
29	139	8.3	234	6	Q28320	Q28320 capra hircu
30	136	8.1	191	6	Q9MYZ2	Q9myz2 capra hircu
31	133.5	8.0	215	11	Q99ND1	Q99nd1 tamiasciuru
32	133	7.9	157	4	O43647	O43647 homo sapien
33	132	7.9	149	4	Q97543	Q97543 aotus nancy
34	132	7.9	217	11	Q9ERG6	Q9erg6 peromyscus
35	131.5	7.9	156	11	Q9IZL4	Q9izl4 sigmodon hi
36	131	7.8	149	6	O97538	O97538 aotus vocif
37	131	7.8	149	6	Q9TTG8	Q9ttg8 aotus nigri
38	130	7.8	204	4	Q96LD2	Q96ld2 homo sapien
39	130	7.8	216	11	O70332	O70332 mesocricetu
40	128.5	7.7	233	6	Q9BEA1	Q9beal tursiops tr
41	127.5	7.6	217	6	Q9BEC5	Q9bec5 tenrec ecau
42	126.5	7.6	217	6	Q9BEG1	Q9beg1 bradypus tr
43	126.5	7.6	217	6	Q9BEG0	Q9beg0 cyclopes di
44	126.5	7.6	250	6	Q9XT47	Q9xt47 macropus eu
45	126	7.5	216	6	Q9BEC9	Q9bec9 ochotona pr

ALIGNMENTS

```
RESULT   1
Q9R1Y0
ID   Q9R1Y0          PRELIMINARY;       PRT;      313 AA.
AC   Q9R1Y0;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   OSTEOCLAST DIFFERENTIATION FACTOR.
GN   TNFSF11.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129;
RX   MEDLINE=99214075; PubMed=10196481;
RA   Kodaira K., Kodaira K., Mizuno A., Yasuda H., Shima N., Murakami A.,
RA   Ueda M., Higashio K.;
RT   "Cloning and characterization of the gene encoding mouse osteoclast
RT   differentiation factor.";
RL   Gene 230:121-127(1999).
DR   EMBL; AB022039; BAA36970.1; -.
DR   EMBL; AB022036; BAA36970.1; JOINED.
DR   EMBL; AB022037; BAA36970.1; JOINED.
DR   EMBL; AB022038; BAA36970.1; JOINED.
DR   HSSP; P50591; 1D0G.
DR   MGD; MGI:1100089; Tnfsf11.
DR   InterPro; IPR003263; TNF_5.
DR   InterPro; IPR000478; TNF_family.
DR   Pfam; PF00229; TNF; 1.
DR   ProDom; PD008600; TNF_5; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS50049; TNF_2; 1.
SQ   SEQUENCE   313 AA;  34719 MW;  37D530BBFC2842E CRC64;

Query Match           98.3%;     Score 1646.5;  DB 11;  Length 313;
Best Local Similarity 99.1%;     Pred. No. 4.3e-139;
```

```
Matches  313;  Conservative  0;  Mismatches  0;  Indels  3;  Gaps  1;

Qy    1  MRRASRDYGKYLRSSEEMGSGSPGVPHEGPLHPAPSAPAPAPPPAASRSMFLALLGLGLGQ  60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1  MRRASRDYGKYLRSSEEMGSGSPGVPHEGPLHPAPSAPAPAPPPAASRSMFLALLGLGLGQ  60

Qy   61  VVCSIALFLYFRAQMDPNRISEDSTHCFYRIRLRHENAGLQDSTLESEDTLPDSCRRMKQ  120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  VVCSIALFLYFRAQMDPNRISEDSTHCFYRIRLRHENAGLQDSTLESEDTLPDSCRRMKQ  120

Qy  121  AFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHK  180
         |||||||||||||||  |||||||||||||||||||||||||||||||||||||||||||
Db  121  AFQGAVQKELQHIVGPQRFS---AMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHK  177

Qy  181  VTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVY  240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  178  VTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVY  237

Qy  241  VVKTSIKIPSSHNLMKGGSTKNWSGNSEEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDP  300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  238  VVKTSIKIPSSHNLMKGGSTKNWSGNSEEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDP  297

Qy  301  DQDATYFGAFKVQDID  316
         ||||||||||||||||
Db  298  DQDATYFGAFKVQDID  313


RESULT 2
Q9ESE2
ID   Q9ESE2      PRELIMINARY;   PRT;   318 AA.
AC   Q9ESE2;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   RECEPTOR ACTIVATOR OF NF-KB LIGAND.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20540945; PubMed=11092398;
RA   Xu J.K., Tan J., Huang L., Gao X.H., Laird R., Liu D., Wysocki S.,
RA   Zheng M.H.;
RT   "Cloning, sequence and functional characterization of the rat
RT   homologue of receptor activator of NF-kB ligand.";
RL   J. Bone Miner. Res. 15:2178-2186(2000).
DR   EMBL; AF187319; AAG17031.1; -.
DR   HSSP; P50591; 1DOG.
DR   InterPro; IPR003263; TNF_5.
DR   InterPro; IPR000478; TNF_family.
DR   Pfam; PF00229; TNF; 1.
DR   ProDom; PD008600; TNF_5; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS50049; TNF_2; 1.
DR   HSSP; P50591; 1DOG.
SQ   SEQUENCE   318 AA;   35370 MW;   4B87A4D706AD098F CRC64;


Query Match   95.3%;   Score  1597;   DB 11;   Length 318;
Best Local Similarity   95.0%;   Pred. No. 1.2e-134;
Matches  302;  Conservative  5;  Mismatches  9;  Indels  2;  Gaps  1;

Qy    1  MRRASRDYGKYLRSSEEMGSGSPGVPHEGPLHPAPSAPAPAPPPAASRSMFLALLGLGLGQ  60
         |||| |||||||| |||||||| |||||||||||||||||| || |||||||||||||||
Db    1  MRRANRDYGKYLRGSEEMGSSCPGVPHEGPLHPAPSAPAPASRAPPAASRFMFLALLGLGLGQ  60

Qy   61  VVCSIALFLYFRAQMDPNRISEDSTHCFYRIRLRHENAGLQDSTLESEDT--LPDSCRRM  118
         |||||||||||||||||||||||||| |||| | |||| |||||||||    ||||||||
Db   61  VVCSIALFLYFRAQMDPNRISEDSTRCFYRILRLRENTGLQDSTLESEDTEALPDSCRRM  120

Qy  119  KQAFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGS  178
         |||||||||| |||||||||||| |||||||||||||| |||||||||||||||| |||||
Db  121  KQAFQGAVQRELQHIVGPQRFSGVPAMMEGSWLDVARRGKPEAQPFAHLTINAADIPSGS  180
```

```
Qy  179  HKVTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLM  238
         |||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  HKVSLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPADYLQLM  240

Qy  239  VYVVKTSIKIPSSHNLMKGGSTKNWSGNSEEFHFYSINVGGFFKLRAGEEISIQVSNPSLL  298
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241  VYVVKTSIKIPSSHNLMKGGSTKNWSGNSEEFHFYSINVGGFFKLRAGEEISIQVSNPSLL  300

Qy  299  DPDQDATYFGAFKVQDID  316
         |||||||||||||||||
Db  301  DPDQDATYFGAFKVQDID  318


RESULT 3
Q9JJK9
ID   Q9JJK9      PRELIMINARY;   PRT;   287 AA.
AC   Q9JJK9;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   RECEPTOR ACTIVATOR OF NF-KB LIGAND 2.
GN   TNFSF11 OR RANKL 2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21150053; PubMed=11250921;
RA   Ikeda T., Kasai M., Utsuyama M., Hirokawa K.;
RT   "Determination of Three Isoforms of the Receptor Activator of Nuclear
RT   Factor-kappaB Ligand and Their Differential Expression in Bone and
RT   Thymus.";
RL   Endocrinology 142:1419-1426(2001).
DR   EMBL; AB032771; BAA97257.1; -.
DR   HSSP; P50591; 1DOG.
DR   MGD; MGI:1100089; Tnfsf11.
DR   InterPro; IPR003263; TNF_5.
DR   InterPro; IPR003636; TNF_abc.
DR   InterPro; IPR000478; TNF_family.
DR   Pfam; PF00229; TNF; 1.
DR   ProDom; PD002012; TNF_abc; 1.
DR   ProDom; PD008600; TNF_5; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS50049; TNF_2; 1.
SQ   SEQUENCE   287 AA;   32234 MW;   8B2CBE4C7B534CC CRC64;


Query Match   88.1%;   Score  1476.5;   DB 11;   Length 287;
Best Local Similarity   90.2%;   Pred. No. 6e-124;
Matches  285;  Conservative  1;  Mismatches  29;  Indels  1;  Gaps  1;

Qy    1  MRRASRDYGKYLRSSEEMGSGSPGVPHEGPLHPAPSAPAPAPPPAASRSMFLALLGLGLGQ  60
         ||||||||||||||                                  ||||||||||||
Db    1  MRRASRDYGKYLRT------------------------------------PASRSMFLALLGLGLGQ  31

Qy   61  VVCSIALFLYFRAQMDPNRISEDSTHCFYRIRLRHENAGLQDSTLESEDTLPDSCRRMKQ  120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   32  VVCSIALFLYFRAQMDPNRISEDSTHCFYRIRLRHENAGLQDSTLESEDTLPDSCRRMKQ  91

Qy  121  AFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHK  180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   92  AFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHK  151

Qy  181  VTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVY  240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  152  VTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVY  211

Qy  241  VVKTSIKIPSSHNLMKGGSTKNWSGNSEEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDP  300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  212  VVKTSIKIPSSHNLMKGGSTKNWSGNSEEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDP  271
```

```
Qy   301 DQDATYFGAFKVQDID 316
         |||||||||||||||
Db   272 DQDATYFGAFKVQDID 287

RESULT  4
ID   Q96Q17;                PRELIMINARY;    PRT;    270 AA.
AC   Q96Q17;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   HRANKL 2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Ikeda T., Kuroyama H., Hirokawa K.;
RT   "Human RANKL isoform.";
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB061227; BAB71768.1; -.
SQ   SEQUENCE  270 AA;  30522 MW;  5C7754CE32E6F368 CRC64;

Query Match             72.8%;   Score 1220;  DB 4;   Length 270;
Best Local Similarity   84.8%;   Pred. No. 4.7e-101;
Matches  229;   Conservative  16;   Mismatches  23;   Indels  2;   Gaps  1;

Qy    49 MFLALLGLGLGQVVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESE 108
         ||:|||||||||||:||| ||||||||||| ||||||| |:||||| |:::|||
Db     1 MFVALLGLGLGQVVCSVALFFYFRAQMDPNRISEDSTHCIYRILRLHENADFQDTTLESQ 60

Qy   109 DT--LPDSCRRMKQAFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAH 166
         ||   |:||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db    61 DTKLIPDSCRRIKQAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAH 120

Qy   167 LTINAASIPSGSHKVTLSSWYHDRGWAKISNMTLSNGKLRVNDGFYYLYANICFRHHET 226
         |||  ||:|||||||| |:||||||||||||||||||||| ||||||||||||||||||
Db   121 LTINATDIPSGSHKVSLSSWYHDRGWAKISNMTFSNGKLIVNDGFYYLYANICFRHHET 180

Qy   227 SGSVPTDYLQLMVYVYVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGE 286
         |||   |:||||||||||||||||| |||| |||||||||||||||||||||||||:||
Db   181 SGDLATEYLQLMVYVYVKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGE 240

Qy   287 EISIQVSNPSLLDPDQDATYFGAFKVQDID 316
         |||:|||||||||||||||||||:|
Db   241 EISIEVSNPSLLDPDQDATYFGAFKVRDID 270
```

```
RESULT  5
ID   Q9JUK8;                PRELIMINARY;    PRT;    199 AA.
AC   Q9JUK8;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   RECEPTOR ACTIVATOR OF NF-KB LIGAND 3.
GN   TNFSF11 OR RANKL 3.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21150053; PubMed=11250921;
RA   Ikeda T., Kasai M., Utsuyama M., Hirokawa K.;
RT   "Determination of Three Isoforms of the Receptor Activator of Nuclear
RT   Factor-kappaB Ligand and Their Differential Expression in Bone and
RT   Thymus.";
RL   Endocrinology 142:1419-1426(2001).
DR   EMBL; AB032772; BAA97258.1; -.
```

```
DR   HSSP; P50591; 1D0G.
DR   MGD; MGI:1100089; Tnfsf11.
DR   InterPro; IPR003263; TNF_5.
DR   InterPro; IPR003636; TNF_abc.
DR   InterPro; IPR000478; TNF_family.
DR   Pfam; PF00229; TNF; 1.
DR   ProDom; PD002012; TNF_abc; 1.
DR   ProDom; PD008600; TNF_5; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS50049; TNF_2; 1.
SQ   SEQUENCE  199 AA;  22150 MW;  4O1C13EB5E8CE166 CRC64;

Query Match             63.1%;   Score 1057;  DB 11;  Length 199;
Best Local Similarity  100.0%;   Pred. No. 1.2e-86;
Matches  199;   Conservative  0;   Mismatches  0;   Indels  0;   Gaps  0;

Qy   118 MKQAFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSG 177
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 MKQAFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSG 60

Qy   178 SHKVTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQL 237
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 SHKVTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQL 120

Qy   238 MVYVVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSL 297
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 MVYVVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSL 180

Qy   298 LDPDQDATYFGAFKVQDID 316
         |||||||||||||||||||
Db   181 LDPDQDATYFGAFKVQDID 199

RESULT  6
ID   Q91ZI9;                PRELIMINARY;    PRT;    53 AA.
AC   Q91ZI9;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   TNFSF11 (FRAGMENT).
GN   TNFSF11.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=F344;
RA   Odgren P.R., Kim N., van Wesenbeeck L., MacKay C.A., Mason-Savas A.,
RA   Safadi F.F., Popoff S.N., Lengner C., van Hul W., Choi Y., Marks S.C.;
RT   "Evidence that the rat osteopetrotic mutation toothless (tl) is not in
RT   the Tnfsf11 (TRANCE, RANKL, ODF, OPGL) gene.";
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF425669; AAL23963.1; -.
FT   NON_TER     1     1
SQ   SEQUENCE  53 AA;  5876 MW;  8A71E32F2B6A9410 CRC64;

Query Match             16.2%;   Score 272;  DB 11;  Length 53;
Best Local Similarity   96.2%;   Pred. No. 2.9e-17;
Matches  51;   Conservative  2;   Mismatches  2;   Indels  0;   Gaps  0;

Qy   264 SGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKVQDID 316
         ||||||||||||||||||||||||||:|||||||||||||||||||||:|
Db     1 SGNSEFHFYSINVGGFFKLRAGEEISVQVSNPSLLDPDQDATYFGAFKVQDMD 53

RESULT  7
ID   Q9DDZ5;                PRELIMINARY;    PRT;    214 AA.
AC   Q9DDZ5;
```

```
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   TRAIL-LIKE PROTEIN.
GN   TNFSF10L.
OS   Brachydanio rerio (Zebrafish) (Zebra danio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC   Cypriniformes; Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Bobe J., Goetz F.W.;
RT   "Molecular cloning and expression of a TNF receptor and two TNF
RT   ligands in the fish ovary.";
RL   Comp. Biochem. Physiol. B, Comp. Biochem. 129:475-481(2001).
DR   EMBL; AF250041; AAG47640.1; -.
DR   HSSP; P50591; 1D0G.
DR   ZFIN; ZDB-GENE-010801-1; tnfsf10l.
DR   InterPro; IPR003263; TNF_5.
DR   InterPro; IPR003636; TNF_abc.
DR   InterPro; IPR000478; TNF_family.
DR   Pfam; PF00229; TNF; 1.
DR   ProDom; PD002012; TNF_abc; 1.
DR   ProDom; PD008600; TNF_5; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS50049; TNF_2; 1.
SQ   SEQUENCE   214 AA;   24093 MW;   98C002474FF691AA CRC64;

Query Match             15.7%;  Score  263.5;  DB 13;  Length 214;
Best Local Similarity   31.5%;  Pred. No. 1.1e-15;
Matches  69;  Conservative  42;  Mismatches  77;  Indels  31;  Gaps  6;

Qy  117 RMKQAFQGAVQKELQHIVGPQRFSGAPAMME-----GS--WLDVAQRGKPEAQPFAHLTI 169
Db    2 KLAEGIKAYISKVTDSIISKQTLHAARTQTHSVNTTGSKFMTTVMQR------PSAHLTL  55

Qy  170 NAASIPS----------------GSHKVTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYL 215
Db   56 SSASDNSRPQSDMHQPQFDLHQSCRHPVHTWANKSFGAHLYNMTLTNGRLRVPQDGRYYL 115

Qy  216 YANICFRHHETSGSVPTDYLQLMVYVV--KTSIKIPSSHNLMKGGSTKNWSGNSEFHFYS 273
Db  116 YSQVYFRYPSPSDSDQSSVSHQLVQCIYKKTSYLNPI--QLLKGVGTKCWAPDAEYALHS 173

Qy  274 INVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKV 312
Db  174 VYQGGLFELRAGDEVFVSVSSPTMVYGEDSSSYFGAFRL 212

RESULT   8
Q90WT9
ID   Q90WT9;      PRELIMINARY;   PRT;   287 AA.
AC   Q90WT9;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   TNF-RELATED APOPTOSIS INDUCING LIGAND.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Bridgham J.T., Johnson A.L.;
RT   "TNF-related apoptosis inducing ligand (TRAIL) expression in the hen
RT   ovary.";
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY057941; AAL23702.1; -.
SQ   SEQUENCE   287 AA;   32092 MW;   DB06E1C95087B108 CRC64;
```

```
Query Match             13.0%;  Score  217.5;  DB 13;  Length 287;
Best Local Similarity   26.7%;  Pred. No. 2.1e-11;
Matches  66;  Conservative  51;  Mismatches  103;  Indels  27;  Gaps  8;

Qy   81 SEDSTHCFYRILRLHENAGLQDSTLESEDTLPDSCRRMKQAFQGAVQKELQHIVGPQRFS 140
Db   51 SSEELRCLQLINQQOEGSNLEE--LISN---QSCLKLANTIKAYVATVTENVISRSVVN 104

Qy  141 GAPAMMEGSWLDVAQ---RGKPEAQPFAHLTI---NAASIPSG--------SHKVTLSSW 186
Db  105 EA---QKSYFNISEGQVATKTLGKPSAHLIFRPQNPAQDGSSRRFGNLSQSCRHAITRW 160

Qy  187 YHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVYV-VKTS 245
Db  161 EDSTIHSHLQNITYRDGRLRVNQAGKYVVYSQIYFRYSRDGAGARVSVPQLVQCINWKTS 220

Qy  246 IKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDAT 305
Db  221 YSQPIL--LLKGVGTKCWAPEAEYGLHALYQGGLFELKAGDELFVSVSSLAIDYSDAAAS 278

Qy  306 YFGAFKV 312
Db  279 YFGAFRL 285

RESULT   9
Q9BDN3
ID   Q9BDN3;      PRELIMINARY;   PRT;   261 AA.
AC   Q9BDN3;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   CD154 PROTEIN.
OS   Callithrix jacchus (Common marmoset).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callithrix.
OX   NCBI_TaxID=9483;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21383618; PubMed=11491535;
RA   Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
RA   Weiss W.R., Ansari A.A.;
RT   "Cloning, sequencing, and homology analysis of nonhuman primate
RT   Fas/Fas-ligand and co-stimulatory molecules.";
RL   Immunogenetics 53:315-328(2001).
DR   EMBL; AF344844; AAK37603.1; -.
DR   HSSP; P29965; 1ALY.
DR   InterPro; IPR003263; TNF_5;
DR   InterPro; IPR000478; TNF_family.
DR   Pfam; PF00229; TNF; 1.
DR   ProDom; PD008600; TNF_5; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
SQ   SEQUENCE   261 AA;   29360 MW;   10CA588D923754EB CRC64;

Query Match             11.3%;  Score  188.5;  DB 6;  Length 261;
Best Local Similarity   25.8%;  Pred. No. 7.3e-09;
Matches  77;  Conservative  49;  Mismatches  110;  Indels  63;  Gaps  16;

Qy   32 PAPSAPAPAPPPAASRSMFLALLGLGLGQVVCSIALF-LYFRAQMDPNRISEDSTHCFYR  90
Db    8 PVPRSAATGPP--VSMKIFMYLLTVFLITQMIGSALFAVYLHRRLD-KIEDER------  57

Qy   91 ILRLHE--------NAGLQDSTLESEDTLPDSCRRMKQAFQGAVQKELQHIVGPQRF 139
Db   58 --NLHEDFVFMKTIQRCNTGERSLSLL------NCEEIKSQFEGFV-KDIM------L 100

Qy  140 SGAPAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHKVTLSSWYHDRGWAKISN-- 197
Db  101 NKEEKKKENSF--EMQKGDQNPQIAAHV-----ISEASSKTSVLQWAEKGYYTMSNNL 152
```

Qy 198 MTLSNGK-LRVNQDGFYLYANICF-RIHETSGSVPTDYLQLMVYVVKTSIKIPSSHN-- 253
          :|:|| |:|| | |::| | | :| | | || | :: :| |:
Db 153 VTLENGKQLTVKRQGLYYIYAQVTFCSNREASSQAP------FIASLCLKPPNRFERI 204

Qy 254 LMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKV 312
         |:: :| |||:| ||| | |:||| | |: |:||| | || |
Db 205 LLRAANTH--SSAKPCGQSIHLGGIFELQPGASVFVNVTDPSQVSHGTGFTSFGLLKL 261

RESULT 10
Q9BDM3
ID   Q9BDM3   PRELIMINARY;   PRT;   261 AA.
AC   Q9BDM3;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   CD154 PROTEIN.
OS   Aotus trivirgatus (Night monkey) (Douroucouli).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
OX   NCBI_TaxID=9505;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21383618; PubMed=11491535;
RA   Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
RA   Weiss W.R., Ansari A.A.;
RT   "Cloning, sequencing, and homology analysis of nonhuman primate
RT   Fas/Fas-ligand and co-stimulatory molecules.";
RL   Immunogenetics 53:315-328(2001).
DR   EMBL; AF344860; AAK37542.1; -.
DR   HSSP; P29965; 1ALY.
DR   InterPro; IPR003263; TNF_5.
DR   InterPro; IPR000478; TNF_family.
DR   Pfam; PF00229; TNF; 1.
DR   ProDom; PD008600; TNF_5; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
SQ   SEQUENCE   261 AA; 29357 MW; 85E1588B507901B5 CRC64;

Query Match   10.9%;
Best Local Similarity   25.8%;
Matches   77; Conservative   49; Mismatches 110; Indels 63; Gaps 16;   Pred. No. 2.5e-08;

Qy   32 PAPSAPAPAPPPAASRMFLALGLGLGQVVCSIALF-LYFRAQMDPNRISEDSTHCFYR 90
          |||| ||| ||| |:|| : ||: | ||: |: ::| | :| | |
Db   8 PAPRSAATGLP--VSMKIFMYLLTVFLLTQMIGSALFAVYLHRRLD--KIEDER------ 57

Qy   91 ILRLHE---------NAGLQDSTLESEDTLPDSCRRMKQAFQGAVQKELQHIVGPQRF 139
          |||| | |::| | | | | |::| |:| | |
Db   58 --NLHEDFVFMKTIQRCNTGERSLSLL------NCEEIKSQFEGFV-KDIM------L 100

Qy 140 SGAPAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHKVTLSSWYHDRGWAKISN-- 197
         | | :| | ||:::: | | |:| |:|:||:|| ||||||||| |:|
Db 101 NKEEKKKENSF--EMQKGDQNPQIAAHV-----ISEASSKTTSVLQWAEKGYYTMSSNNL 152

Qy 198 MTLSNGK-LRVNQDGFYLYANICF-RIHETSGSVPTDYLQLMVYVVKTSIKIPSSHN-- 253
          :|:|| |:|| | |::| | | :| | | || | :: :| |:
Db 153 VTLENGKQLTVKRQGLYYIYAQVTFCSNREASSQAP------FIASLCLKPPNRFERI 204

Qy 254 LMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKV 312
         |:: :| |||:| ||| | |:||| | |: |:||| | || |
Db 205 LLRAANTH--SSAKPCGQSIHLGGIFELQPGASVFVNVTDPSQVSHGTGFTSFGLLKL 261

RESULT 11
Q9BEA8
ID   Q9BEA8   PRELIMINARY;   PRT;   282 AA.
AC   Q9BEA8;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   FAS-LIGAND (FAS LIGAND).
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21322533; PubMed=11429161;
RA   Muneta Y., Shimoji Y., Inumaru S., Mori Y.;
RT   "Molecular cloning, characterization, and expression of porcine Fas
RT   ligand (CD95 ligand).";
RL   J. Interferon Cytokine Res. 21:305-312(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Tsuyuki S., Kono M., Bloom E.T.;
RT   "Cloning and potential utility of porcine Fas ligand: overexpression
RT   in porcine cells protects them from attack by human cytolytic cells.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB027297; BAB40919.1; -.
DR   EMBL; AF397407; AAK84408.1; -.
DR   HSSP; P01375; 4TSV.
DR   InterPro; IPR003263; TNF_5.
DR   InterPro; IPR003636; TNF_abc.
DR   InterPro; IPR000478; TNF_family.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   ProDom; PD002012; TNF_abc; 1.
DR   ProDom; PD008600; TNF_5; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
SQ   SEQUENCE   282 AA; 31756 MW; 6743DAA1145671FB CRC64;

Query Match   10.7%;
Best Local Similarity   21.6%;   Pred. No. 5.1e-08;
Matches 105; Conservative   42; Mismatches 107; Indels 70; Gaps 10;

Qy   20 SGPGVPHEGPLHPAPSAPAPAPPPAASRS-----------------------------MF 50
          || | | | ||| |||| |||||:
Db   35 SVPGRP--GQRRPPPPPPPPPPPPTLLFSRPLPLPPPSLKKKRDHNAGLCLLVMFFMVL 92

Qy   51 LALLGLGLGQVVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESEDT 110
         :||:|||| | | : ::| | |:|:
Db   93 VALVGLGLG----------MFQLFHLQKE--------------LTELRESASQRHT------ 124

Qy 111 LPDSCRRMKQAFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLT-- 168
         | :|: | | | ||:: |:|
Db 125 -----------------ESSLEKQIGHPNLPSE--------------------KKELRKVAHLTGK 153

Qy 169 INAASIPSGSHKVTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSG 228
          : || | | ||:|:| |: :: :|
Db 154 PNSRSIP------LEWEDTYGIALVSGVKYMKGSLVINDTGLYFVYSKVYFRGQYCNN 205

Qy 229 SVPTDYLQLMVYVVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEI 288
         | :   ::: |:| | | | :
Db 206 Q------PLSHKYYTRNSRYPQDLVLME-GKMMNYCTTGQMARSSYLGAVFNLTSADHL 258

Qy 289 SIQVSNPSLLDPDQDATYFGAFKV 312
         ||| |:||| | || |
Db 259 YVNVSELSLVNFEESKTFFGLYKL 282

RESULT 12
Q95M04
ID   Q95M04   PRELIMINARY;   PRT;   282 AA.
AC   Q95M04;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   FAS-LIGAND.
GN   FASL.

DR   ProDom; PD002012; TNF_abc; 1.
DR   ProDom; PD008600; TNF_5; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
SQ   SEQUENCE 280 AA; 31377 MW; 729EA6143GF2D398 CRC64;

Query Match   10.7%; Score 179; DB 6; Length 280;
Best Local Similarity 21.3%; Pred. No. 5.6e-08;
Matches 67; Conservative 43; Mismatches 107; Indels 98; Gaps   9;

Qy   22 PGVPHEGPLHPAPSAPAPPPAASRSM---------------------------FLALLGLGLG   59
            || | | | ||||| ||:|:||||
Db   40 PGQRRPPPPPPPPPPLPPPPPPLPPPLPPPLKKRGNHSTGLCLLVMFFMVVALVGLGLG   99

Qy   60 QVVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLPDSCRRMK 119
            :|:
Db   100 ------MFQLFHLQ-------------------------KELAELRESTSQKHTA- 123

Qy   120 QAFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLT--INAASIPSG 177
            :::|:|: | :|
Db   124 ----SSLEKQIGHPSPPPE-----------------KKEQRKVAHLTGKPNSRSMP-- 158

Qy   178 SHKVTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYLYANICFRHHETSGSSVPTDYLQL 237
            |||
Db   159 ------LEWEDTYGIVLLSGVKYKKGGLVINETGLYFVYSKVYFRGQSCTN-----LPL 206

Qy   238 MVYVVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSL 297
            : | :
Db   207 SHKVYMRNSKYPQDLVMME-GKMMSYCTTGQMWAHSSYLGAVFNLTSADHLYVNVSELSL 265

Qy   298 LDPDQDATYFGAFKV 312
            :: ||: |:|
Db   266 VNFEESQTFFGLYKL 280

RESULT 14
Q95N10
ID   Q95N10;   PRELIMINARY;   PRT;   282 AA.
AC   Q95N10;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   FAS LIGAND.
GN   FASL.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Zhu N., Young Y.;
RT   "Molecular cloning and characterization of porcine Fas ligand cDNA.";
RL   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY033634; AAK56449.1; -.
SQ   SEQUENCE 282 AA; 31752 MW; F39121240GAE1E7D CRC64;

Query Match   10.7%; Score 178.5; DB 6; Length 282;
Best Local Similarity 21.6%; Pred. No. 6.3e-08;
Matches 70; Conservative 42; Mismatches 105; Indels 107; Gaps 10;

Qy   20 SGPGVPHEGPLHPAPSAPAPPPAASRS-----------------------MF   50
            | ||| | | |||||
Db   35 SVPGRP--GQRRPPPPPPPPPPPPLLPSRPLPPPLPPPSLKKKRDHNAGLCLLVMFFMVL   92

Qy   51 LALLGLGLGQVVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESEDT 110
            :|:|:||||
Db   93 VALVGLGLG------MFQLFHLQKE----------LTELRESASQRHT---------- 124

Qy   111 LPDSCRRMKQAFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLT-- 168

OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BREED LANDRACE X LARGE YORKSHIRE WHITE (LW); TISSUE=LIVER;
RA   Motegi-Ishiyama Y., Nakajima Y., Hoka S., Takagaki Y.;
RT   "Genomic Sequence Analysis of Pig Fas-Ligand Gene.";
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB069764; BAB64291.1; -. E5474EBF455127B CRC64;
SQ   SEQUENCE 282 AA; 31722 MW; E5474EBF455127B CRC64;

Query Match   10.7%; Score 179.5; DB 6; Length 282;
Best Local Similarity 21.6%; Pred. No. 5.1e-08;
Matches 70; Conservative 42; Mismatches 105; Indels 107; Gaps 10;

Qy   20 SGPGVPHEGPLHPAPSAPAPPPAASRS-----------------------MF   50
            | ||| | | |||||
Db   35 SVPGRP--GQRRPPPPPPPPPPTLLPSRPLPPPLPPPSLKKKRDHNAGLCLLVMFFMVL   92

Qy   51 LALLGLGLGQVVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESEDT 110
            :|:|:||||
Db   93 VALVGLGLG------MFQLFHLQKE----------LTELRESASQRHT---------- 124

Qy   111 LPDSCRRMKQAFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLT-- 168
            | | |
Db   125 -----------ESSLEKQIGHPNLPSE---------------KKELRKVAHLTGK 153

Qy   169 INAASIPSGSHKVTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYLLYANICFRHHETSG 228
            : :| :
Db   154 -------LEWEDTYGIALVSGVKYMKGSLVINDTGLYFVYSKVYFRGQYCNN 205

Qy   229 SVPTDYLQLMVYVVKTSIKIPSSHNLMKGGSTKNWSGNSEFHYSINVGGFFKLRAGEEI 288
            | : | |
Db   206 Q------PLSHKVYTRNSRYPQDLVLME-GKMMNYCTTGQMWARSSYLGAVFNLTSADHL 258

Qy   289 SIQVSNPSLLDPDQDATYFGAFKV 312
            :|::| :: :|:|: |:|
Db   259 YVNVSELSLVNFEESKTFFGLYKL 282

RESULT 13
Q9BDM5
ID   Q9BDM5;   PRELIMINARY;   PRT;   280 AA.
AC   Q9BDM5;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   FAS ANTIGEN CD95.
OS   Macaca mulatta (Rhesus macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9544;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21383618; PubMed=11491535;
RA   Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
RA   Weiss W.R., Ansari A.A.;
RT   "Cloning, sequencing, and homology analysis of nonhuman primate
RT   Fas/Fas-ligand and co-stimulatory molecules.";
RL   Immunogenetics 53:315-328(2001).
DR   EMBL; AF344856; AAK37539.1; -.
DR   HSSP; P01375; 4TSV.
DR   InterPro; IPR002965; P_rich_extensn.
DR   InterPro; IPR003263; TNF_5.
DR   InterPro; IPR003636; TNF_abc.
DR   InterPro; IPR000478; TNF_family.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01217; PRICHEXTENSN.
DR   PRINTS; PR01234; TNECROSISFCT.

```
Db    125 ----------------ESSLEKQIGHPNLPSE----------------KKELRKVAHLTGK 153

Qy    169 INAASIPSGSHKVTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSG 228
          |: ||                          :
Db    154 PNSRSIP--------LEWEDTYGIALVSGVKYMKGSLVINDTGLYFVYSKVYFRGQYCNN 205

Qy    229 SVPTDYLQLMVYYVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEI 288
             |      ||  ||    |  :  || |  ||::| :||:||
Db    206 Q------PLSHKVTRNSRYPQDLVLME-GKMMNYCTTGQMWARSSYLGAVFNLTSADHL 258

Qy    289 SIQVSNPSLLDPDQDATYFGAFKV 312
          : |   ||:|:    |:||:|
Db    259 YVNVSELSLVNFEESKTFFGLYKL 282
```

RESULT 15
Q9MYL6
```
ID   Q9MYL6        PRELIMINARY;          PRT;      280 AA.
AC   Q9MYL6;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   FAS LIGAND.
GN   PT-FASL OR CM-FASL OR RM-FASL.
OS   Macaca nemestrina (Pig-tailed macaque),
OS   Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey), and
OS   Macaca mulatta (Rhesus macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9545, 9541, 9544;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   SPECIES=M.nemestrina; STRAIN=PIG-TAILED MONKEY;
RA   Kiril Y., Inoue T., Yoshino K.;
RT   "Pig-tailed monkey Fas ligand mRNA, complete cds.";
RL   Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   SPECIES=M.fascicularis; STRAIN=CYNOMOLGUS MONKEY;
RA   Kiril Y., Inoue T., Yoshino K.;
RT   "Cynomolgus monkey Fas ligand mRNA, complete cds.";
RL   Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   SPECIES=M.mulatta; STRAIN=RHESUS MONKEY;
RA   Kiril Y., Inoue T., Yoshino K.;
RT   "Rhesus monkey Fas ligand mRNA, complete cds.";
RL   Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB035140; BAA90296.1; -.
DR   EMBL; AB035138; BAA90294.1; -.
DR   EMBL; AB035139; BAA90295.1; -.
DR   HSSP; P01375; 4TSV.
DR   InterPro; IPR003263; TNF_5.
DR   InterPro; IPR003636; TNF_abc.
DR   InterPro; IPR000478; TNF_family.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSLSFCT.
DR   ProDom; PD002012; TNF_abc; 1.
DR   ProDom; PD008600; TNF_5; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
SQ   SEQUENCE   280 AA;   31367 MW;   F0B284D61A132EB4 CRC64;

Query Match             10.6%;  Score 178;  DB 6;  Length 280;
Best Local Similarity   22.0%;  Pred. No. 6.9e-08;
Matches   68;  Conservative   44;  Mismatches  105;  Indels   92;  Gaps   10;

Qy    22 PGVPHEGPLHPAPSAPAP--APPPAASRS--------------MFLALLGLGLGQVVCSI 65
          |  |  ||:| ||:| ||  ||||    :            :: |:||:|||||
Db    46 PPPPPPPLPPPPPPSPLPPLPLPLKKRGNHSTGLCLLVMFFMVLVALVGLGLG------ 99
```

```
Qy    66 ALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESEDTLPDSCRRMKQAFQGA 125
             :| |   |                                  |:|:::||:
Db   100 -MFQLFHLQ--------------------------KELAELRESTSQKHTA--------SS 125

Qy   126 VQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLT--INAASIPSGSHKVTL 183
          ::|::|  |                            ||  ||||  :::::||
Db   126 LEKQIGHPSPPPE----------------------KKEQRKVAHLTGKPNSRSMP----- 158

Qy   184 SSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVYYVVK 243
          |||  ::|  |  :|  | |  :  |::|||  :|:  :|  ||
Db   159 LEWEDTYGIVLLSGVKYKKGGLVINETGLYFVYSKVYFRGQSCTN-----LPLSHKVYM 212

Qy   244 TSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQD 303
              :|     :|    ::|:|::|||  :|||  ||  ||:
Db   213 RNSKYPQDLVMME-GKMMSYCTTGQMWAHSSYLGAVFNLTSADHLYVNVSELSLVNFEES 271

Qy   304 ATYFGAFKV 312
          :|:|| :|:
Db   272 QTFFGLYKL 280
```

Search completed: July 15, 2002, 11:05:29
Job time: 239 sec

us-09-671-658a-2.rspt

```
            GenCore version 4.5
     Copyright (c) 1993 - 2000  Compugen Ltd.

OM protein - protein search, using sw model

Run on:    July 15, 2002, 11:01:05 ; Search time 17.53 Seconds
                                      (without alignments)
                                      1732.129 Million cell updates/sec

Title:           US-09-671-658A-2
Perfect score:   1675
Sequence:        1 MRRASRDYGKYLRSSEEMGS........LLDPDQDATYFGAFKVQDID 316

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        283138 seqs, 96089334 residues

number of hits satisfying chosen parameters:     283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       PIR_71:*
                 1: Pir1:*
                 2: pir2:*
                 3: pir3:*
                 4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
```

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	185.5	11.1	261	2	S53090	CD40 ligand - bovi
2	183	10.9	278	2	A49266	fas ligand - rat
3	182	10.9	279	2	A53062	Fas ligand - mouse
4	173.5	10.4	281	2	I38707	Fas ligand - human
5	171.5	10.2	261	2	I53476	CD40 ligand - huma
6	157	9.4	260	2	S21738	CD40 ligand - mous
7	149	8.9	234	1	JQ1344	tumor necrosis fac
8	146.5	8.7	235	1	QWMSN	tumor necrosis fac
9	143.5	8.6	233	2	S22052	tumor necrosis fac
10	141	8.4	234	1	JH0529	tumor necrosis fac
11	140	8.4	233	2	S11688	tumor necrosis fac
12	139.5	8.3	233	1	QWHUN	tumor necrosis fac
13	137.5	8.2	234	1	A25451	tumor necrosis fac
14	135.5	8.1	235	1	I54490	tumor necrosis fac
15	133.5	8.0	233	1	S24642	tumor necrosis fac
16	133	7.9	185	2	S52715	tumor necrosis fac
17	133	7.9	232	1	S12606	tumor necrosis fac
18	129.5	7.7	235	2	JU0029	tumor necrosis fac
19	129.5	7.7	306	2	I49139	lymphotoxin-beta -
20	117	7.0	244	2	A46066	lymphotoxin beta -
21	115.5	6.9	193	2	S06192	tumor necrosis fac
22	103.5	6.2	340	2	S49742	hypothetical prote
23	103	6.1	3848	2	T17414	TipC protein - sli
24	99.5	5.9	558	2	T23649	hypothetical prote
25	99	5.9	440	2	I49681	glyceraldehyde-3-p
26	97	5.8	450	2	S38114	hypothetical prote
27	95.5	5.7	553	2	B55514	dihydrolipoamide S
28	94	5.6	1486	1	B40333	collagen alpha 1(I
29	93.5	5.6	205	1	QWHUX	lymphotoxin alpha
30	92.5	5.5	197	1	JH0309	tumor necrosis fac
31	92	5.5	549	2	JC5926	secreted klotho pr
32	92	5.5	785	2	T23456	hypothetical prote
33	92	5.5	1012	2	JC5925	membrane klotho pr
34	90.5	5.4	658	2	T39500	serine/threonine-s
35	90.5	5.4	750	2	E84475	probable Athila re
36	90.5	5.4	952	2	AC0447	probable insecti
37	90	5.4	3011	1	S40770	genome polyprotein
38	89	5.3	1694	2	S50065	sialoadhesin - mou
39	88.5	5.3	202	1	B27303	tumor necrosis fac
40	88.5	5.3	477	2	I38409	adenylyl cyclase-a
41	88.5	5.3	1547	2	JQ0096	hypothetical 176K
42	88	5.3	347	2	H75253	hypothetical prote
43	88	5.3	560	1	JQ1221	probable 60K inner
44	88	5.3	1420	2	T37781	probable cytoskele
45	88	5.3	2774	2	A43359	microtubule-associ

ALIGNMENTS

```
RESULT  1
S53090
CD40 ligand - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 05-Nov-1999
C;Accession: S53090
R;Mertens, B.E.L.C.; Muriuki, M.
submitted to the EMBL Data Library, February 1995
A;Description: Cloning of bovine CD40L and homology to bovine TNFA and TNFB.
A;Reference number: S53090
A;Accession: S53090
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-261 <MER>
A;Cross-references: EMBL:Z48469; NID:g732569; PIDN:CAA88363.1; PID:g732570

Query Match            11.1%;   Score 185.5;  DB 2;  Length 261;
Best Local Similarity  25.1%;   Pred. No. 5.4e-08;
Matches 75; Conservative 50; Mismatches 111; Indels 63; Gaps 15;

Qy   32 PAPSAPAPAPPPRAASRSMFLALLGLGLGQVVCSIALF-LYFRAQMDPNRISEDSTHCFYR 90
         |:|:||:| ::| ::|:||: :||  ||| :||  ::| |:::|   ::| :|:|| :
Db    8 PSPRSVATGPP--VSMKIFMYLLTVFLITQMIGSALFAVYLHRRLD--KIEDER------ 57

Qy   91 ILRLHE---------NAGLQDSTLESEDTLPDSCRRMKQAFQGAVQKELQHIVGPQRF 139
              |||           | | |   :||::|:  :| :: :
Db   58 --NLHEDFVFMKTIQRCNKGEGSLSLL-------NCEEIRSRFEDLVKDIMQN---KEV 104

Qy  140 SGAPAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHKVTLSSWYHDRGWAKISN- 197
                 :||:  | ||  ||   |            ||
Db  105 KKKEKNFE------MHKGDQEPQIAAHV-----ISEASSKTTSVLQWAPKGYTLSNNL 152

Qy  198 MTLSNGK-LRVNQDGFYYLYANICF-RHHETSGSVPTDYLQLMVYVVKTSIKIPSSHN- 253
         :|:||:| ::||||:| |: ||:|            ::  :|
Db  153 VTLENGKQLAVKRQGFYYIYTQVTFCSNRETLSQAP-----FIASLCLKSPSGSERI 204

Qy  254 LMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKV 312
         |:: :| ::| || :  ||||:||| :|||:|: :| |:| |::|||||||||||:||
Db  205 LLRAANTH--SSSKPCGQGSIHLGGVFELQSGASVFVNVTDPSQVSHGTGFTSFGLLKL 261

RESULT  2
A49266
fas ligand - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C;Accession: A49266
R;Suda, T.; Takahashi, T.; Golstein, P.; Nagata, S.
Cell 75, 1169-1178, 1993
A;Title: Molecular cloning and expression of the Fas ligand, a novel member of the tu
A;Reference number: A49266; MUID:94084792
```

A;Accession: A49266
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-278 <SUD>
C;Cross-references: GB;U03470; NID:g440178; PIDN:AAC52129.1; PID:g440179
C;Keywords: glycoprotein; transmembrane protein

Query Match   10.9%; Score 183; DB 2; Length 278;
Best Local Similarity   23.4%; Pred. No. 9.5e-08;
Matches 75; Conservative 42; Mismatches 107; Indels 96; Gaps 13;

```
Qy   14  SSEEMGSG-----PGVPHEGPLHPAPSAPAPAPP----------PAASRSMFLALL   54
             |  ||      || |   | | |    || |           :  ||| |:
Db   34  SSGPRGPGQRRPPPPPPPSPL-PPPSQPPLPLPPLPLKKKDNIELWLPVIFFMVLVALV  92

Qy   55  GLGLGQVVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESEDTLPDS 114
         |:|||      :|||||| | |                                :|:
Db   93  GMGLG------MYQLFHLQKELAELREFTNH-----------SLRVSSFEKQIANPST 133

Qy  115  CRRMKQAFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLTIN--AA 172
                                                            |: ||||  :
Db  134  PSETK-------------------------------------KPRS--VAHLTGNPRSR 153

Qy  173  SIPSGSHKVTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPT 232
         ||:         |:|| :||  : || |    ||| || :|:|:|  || :||  :|:|:
Db  154  SIP-------LEWEDTYGTALISGVKYKKGGLVINEAGLYFVYSKYFR-GQSCNSQP- 203

Qy  233  DYLQLMVVVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQV 292
           :| || |  |      :| ||   :  || |   :| ||  |||| |:  ||:|:|:|
Db  204  --LSHKVYM--RNFKYPGDLVLME-EKKLNYCTTGQIWAHSSYLGAVFNLTVADHLYVNI 258

Qy  293  SNPSLLDPDQDATYFGAFKV 312
         | :: :|  : :|||| :| :
Db  259  SQLSLINFEESKTFFGLYKL 278
```

RESULT 3
A53062
Fas ligand - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C;Accession: A53062
R;Takahashi, T.; Tanaka, M.; Brannan, C.I.; Jenkins, N.A.; Copeland, N.G.; Suda, T.; Nag
Cell 76, 969-976, 1994
A;Title: Generalized lymphoproliferative disease in mice, caused by a point mutation in
A;Reference number: A53062; MUID:94185175
A;Accession: A53062
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-279 <TAK>
A;Cross-references: GB;U06948; NID:g473564; PIDN:AAA17800.1; PID:g473565

Query Match   10.9%; Score 182; DB 2; Length 279;
Best Local Similarity   22.7%; Pred. No. 1.2e-07;
Matches 72; Conservative 48; Mismatches 105; Indels 92; Gaps 13;

```
Qy   13  RSSEEMGSGPGVPHEGPLHPAPSAPAPAPP-----------PAASRSMFLALLGLGLG   57
          |  ||||| || |   | | |    || |           :  ||| |: || |:
Db   38  RGPDQRRPPPPPPPVSPL-PPPSQPLPLPPLTPLKKKDHNTNLWLPVVFFMVLVALVGMG  96

Qy   58  LGQVVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESEDTLPDSCRR 117
         ||      :|||||| |                             :|:
Db   97  LG------MYQLFHLQKE---LAE----LREFTNQSLKVSSFEKQIANPST--- 134

Qy  118  MKQAFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLTIN--AASIP 175
                                                         |: ||||  :|:|
Db  135  ---------------------PSE--------------KKEPRSVAHLTGNPHSRSIP 157

Qy  176  SGSHKVTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYL 235
          ||         |:|| :||  : || |    ||| || :|:|:|  || :|| :|:|::|
Db  158  --LEWEDTYGTALISGVKYKKGGLVINETGLYFVYSKVYFR-GQSCNNQPLNH- 207
```

```
Qy  236  QLMVYVVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNP 295
          :|  || |  |      :| ||   :  || |   :| ||  |||| |:  ||:|:|: |
Db  208  --KVYM--RNSKYPEDLVLME-EKRLNYCTTGQIWAHSSYLGAVFNLTSADHLYVNISQL 262

Qy  296  SLLDPDQDATYFGAFKV 312
          : :| : :|||| :| :
Db  263  SLINFEESKTFFGLYKL 279
```

RESULT 4
I38707
Fas ligand - human
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C;Accession: I38707; JC2340; S57565; I38554
R;Takahashi, T.; Tanaka, M.; Inazawa, J.; Abe, T.; Suda, T.; Nagata, S.
Int. Immunol. 6, 1567-1574, 1994
A;Title: Human Fas ligand: gene structure, chromosomal location and species specifici
A;Reference number: I38707; MUID:95127560
A;Accession: I38707
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-281 <RES>
A;Cross-references: EMBL;U11821; NID:g595430; PIDN:AAC50124.1; PID:g595431
R;Mita, E.; Hayashi, N.; Iio, S.; Takehara, T.; Hijioka, T.; Kasahara, A.; Fusamoto,
Biochem. Biophys. Res. Commun. 204, 468-474, 1994
A;Title: Role of Fas ligand in apoptosis induced by hepatitis C virus infection.
A;Reference number: JC2340; MUID:95071350
A;Accession: JC2340
A;Molecule type: DNA
A;Residues: 1-281 <MIT>
A;Cross-references: GB;D38122; DDBJ:D29820; NID:g601892; PIDN:BAA07320.1; PID:g136990
R;Schatzlein, C.E.
submitted to the EMBL Data Library, June 1995
A;Reference number: S57565
A;Accession: S57565
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-281 <SCH>
A;Cross-references: EMBL;X89102; NID:g887455; PID:g887456
R;Alderson, M.R.; Tough, T.W.; Davis-Smith, T.; Braddy, S.; Falk, B.; Schooley, K.A.;
J. Exp. Med. 181, 71-77, 1995
A;Title: Fas ligand mediates activation-induced cell death in human T lymphocytes.
A;Reference number: I38554; MUID:95105731
A;Accession: I38554
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-281 <RE2>
A;Cross-references: EMBL;U08137; NID:g624627; PIDN:AAC50071.1; PID:g624628
C;Genetics:
A;Gene: FasL
A;Introns: 151/1; 116/3
C;Keywords: glycoprotein; transmembrane protein
F;80-102/Domain: transmembrane #status predicted <TMM>
F;76,184,250,260/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match   10.4%; Score 173.5; DB 2; Length 281;
Best Local Similarity   21.2%; Pred. No. 5e-07;
Matches 67; Conservative 42; Mismatches 108; Indels 99; Gaps   9;

```
Qy   22  PGVPHEGPLHPAPSAPAPAPPAASR-----------SMFLALLGLGL  58
         || |   | | |    || |    :           ||:||| |: :
Db   40  PGQRRPPPPPPPPPLPPPPPPPLPLPPLPLKKKRGNHSTGLCLLVMFFMVLVALVGLGL  99

Qy   59  GQVVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESEDTLPDSCRRM 118
         |:      |||:|  |
Db  100  G-----MYQLFHLQ-------------------------------KELAELRESTSQMHTA- 124

Qy  119  KQAFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLT--INAASIPS 176
                :|::|  | | |                        |: ||||  |:||:|:
Db  125  ----SSLEKQIGHPSPPPE-----------------------KKELRKVAHLTGKSNSRSMP- 159
```

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 15, 2002, 11:01:55 ; Search time 13.43 Seconds
                                          (without alignments)
                                          911.048 Million cell updates/sec

Title: US-09-671-658A-2
Perfect score: 1675
Sequence: 1 MRRASRDYGKYLRSSEEMGS.........LLDPDQDATYFGAFKVQDID 316

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
          score greater than or equal to the score of the result being printed,
          and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1675	100.0	316	1	TN11_MOUSE	O35235 m tumor nec
2	1417.5	84.6	317	1	TN11_HUMAN	O14788 h tumor nec
3	258.5	15.4	281	1	TN10_HUMAN	P50591 homo sapien
4	244	14.6	291	1	TN10_MOUSE	P50592 mus musculu
5	185.5	11.1	261	1	TNF5_BOVIN	P51749 bos taurus
6	183	10.9	278	1	FASL_RAT	P36940 rattus norv
7	182	10.9	279	1	FASL_MOUSE	P41047 mus musculu
8	173.5	10.4	281	1	FASL_HUMAN	P48023 homo sapien
9	171.5	10.2	261	1	TNF5_HUMAN	P29965 homo sapien
10	164	9.8	260	1	TNF5_FELCA	O97605 felis silve
11	157	9.4	234	1	TNF5_CAVPO	P51435 cavia porce
12	157	9.4	260	1	TNF5_MOUSE	P27548 mus musculu
13	154	9.2	260	1	TNF5_CANFA	O97626 canis famil
14	149	8.9	234	1	TNFA_HORSE	P29553 equus cabal
15	148.5	8.9	233	1	TNFA_MACFA	P79337 macaca fasc
16	147.5	8.8	233	1	TNFA_MACMU	P48094 macaca mula
17	146.5	8.7	235	1	TNFA_MOUSE	P06804 mus musculu
18	143.5	8.6	233	1	TNFA_PAPHU	O77510 papio hamad
19	143.5	8.6	233	1	TNFA_PAPSP	P33620 papio sp. (
20	141	8.4	234	1	TNFA_SHEEP	P23383 ovis aries
21	140	8.4	233	1	TNFA_FELCA	P19101 felis silve
22	139.5	8.3	233	1	TNFA_CANFA	P51742 canis famil
23	139.5	8.3	233	1	TNFA_RABIT	P01375 homo sapien
24	137	8.2	235	1	TNFA_RABIT	P04924 oryctolagus
25	135.5	8.1	235	1	TNFA_PERLE	P36939 peromyscus
26	134.5	8.0	240	1	TN14_HUMAN	O43557 homo sapien
27	133.5	8.0	233	1	TNFA_BOVIN	Q06599 bos taurus
28	133	7.9	232	1	TNFA_PIG	P23563 sus scrofa
29	129.5	7.7	233	1	TNFA_MARMO	O35734 marmota mon
30	129.5	7.7	235	1	TNFA_RAT	P16599 rattus norv
31	129.5	7.7	306	1	TNFC_MOUSE	P41155 mus musculu
32	128	7.6	229	1	TNFC_CEREL	P51743 cervus elap
33	117	7.0	244	1	TNFC_HUMAN	Q06643 homo sapien
34	115.5	6.9	193	1	TNFA_CAPHI	P13296 capra hircu
35	109.5	6.5	233	1	TNFA_MACEU	O77764 macropus eu
36	109	6.5	201	1	TNFB_MACEU	Q9xt48 macropus eu
37	103.5	6.2	340	1	YMD7_YEAST	Q03703 saccharomyc
38	99	5.8	440	1	G3PT_MOUSE	Q64467 mus musculu
39	97	5.7	450	1	YK22_YEAST	P36135 saccharomyc
40	95.5	5.6	553	1	ODP2_ALCEU	Q59098 alcaligenes
41	93.5	5.6	205	1	TNFB_HUMAN	P01374 homo sapien
42	92.5	5.5	197	1	TNFB_RABIT	P10154 oryctolagus
43	91	5.5	616	1	SPAS_HUMAN	Q9ubp0 homo sapien
44	90.5	5.4	658	1	PAK1_SCHPO	P50527 schizosacch
45	89	5.3	1694	1	SN_MOUSE	Q62230 mus musculu

ALIGNMENTS

RESULT   1
TN11_MOUSE
ID   TN11_MOUSE   STANDARD;   PRT;   316 AA.
AC   O35235; O35306;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Tumor necrosis factor ligand superfamily member 11 (Receptor activator
DE   of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-
DE   induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteoclast
DE   differentiation factor) (ODF) (Osteoclastogenesis-inhibitory factor)
DE   (OCIF).
GN   TNFSF11 OR RANKL OR TRANCE OR OPGL.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Hybridoma;
RX   MEDLINE=97460112; PubMed=9312132;
RA   Wong B.R., Rho J., Arron J., Robinson E., Orlinick J., Chao M.,
RA   Kalachikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee S.Y.,
RA   Choi Y.;
RT   "TRANCE is a novel ligand of the tumor necrosis factor receptor family
RT   that activates c-Jun N-terminal kinase in T cells.";
RL   J. Biol. Chem. 272:25190-25194(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Bone marrow;
RX   MEDLINE=98227661; PubMed=9568710;
RA   Lacey D.L., Timms E., Tan H.-L., Kelley M.J., Dunstan C.R.,
RA   Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hsu H.,
RA   Sullivan J., Hawkins N., Davy E., Capparelli C., Eli A., Qian Y.-X.,
RA   Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J.,
RA   Boyle W.J.;
RT   "Osteoprotegerin ligand is a cytokine that regulates osteoclast
RT   differentiation and activation.";
RL   Cell 93:165-176(1998).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Bone marrow stroma;
RX   MEDLINE=98188248; PubMed=9520411;
RA   Yasuda H., Shima N., Nakagawa N., Yamaguchi K., Kinosaki M.,
RA   Mochizuki S.-I., Tomoyasu A., Yano K., Goto M., Murakami A., Tsuda E.,
RA   Morinaga T., Higashio K., Udagawa N., Takahashi N., Suda T.;
RT   "Osteoclast differentiation factor is a ligand for
RT   osteoprotegerin/osteoclastogenesis-inhibitory factor and is identical
RT   to TRANCE/RANKL.";
RL   Proc. Natl. Acad. Sci. U.S.A. 95:3597-3602(1998).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Thymic lymphoma;
RX   MEDLINE=98032977; PubMed=9367155;
RA   Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
RA   Tometsko M.E., Roux E.R., Teepe M.C., DuBose R.F., Cosman D.,

```
Qy  121 AFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHK 180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 AFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHK 180

Qy  181 VTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVY 240
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 VTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVY 240

Qy  241 VVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDP 300
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 VVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDP 300

Qy  301 DQDATYFGAFKVQDID 316
        ||||||||||||||||
Db  301 DQDATYFGAFKVQDID 316
```

RESULT 2
TN11_HUMAN
ID   TN11_HUMAN   STANDARD;   PRT;   317 AA.
AC   O14788; O14723; Q9P2Q3;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Tumor necrosis factor ligand superfamily member 11 (Receptor activator
DE   of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-
DE   induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteoclast
DE   differentiation factor) (ODF).
GN   TNFSF11 OR RANKL OR TRANCE OR OPGL.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Bone marrow, and Peripheral blood;
RX   MEDLINE=98032977; PubMed=9367155;
RA   Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
RA   Tometsko M.E., Roux E.R., Teepe M.C., DuBose R.F., Cosman D.,
RA   Galibert L.;
RT   "A homologue of the TNF receptor and its ligand enhance T-cell growth
RT   and dendritic-cell function.";
RL   Nature 390:175-179(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymph node;
RX   MEDLINE=98227661; PubMed=9568710;
RA   Lacey D.L., Timms E., Tan H.-L., Kelley M.J., Dunstan C.R.,
RA   Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hsu H.,
RA   Sullivan J., Hawkins N., Davy E., Capparelli C., Eli A., Qian Y.-X.,
RA   Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J.,
RA   Boyle W.J.;
RT   "Osteoprotegerin ligand is a cytokine that regulates osteoclast
RT   differentiation and activation.";
RL   Cell 93:165-176(1998).
RN   [3]
RP   SEQUENCE OF 73-317 FROM N.A.
RC   TISSUE=Thymocytes;
RX   MEDLINE=97460112; PubMed=9312133;
RA   Wong B.R., Rho J., Arron J., Robinson E., Orlinick J., Chao M.,
RA   Kalachikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee S.Y.,
RA   Choi Y.;
RT   "TRANCE is a novel ligand of the tumor necrosis factor receptor family
RT   that activates c-Jun N-terminal kinase in T cells.";
RL   J. Biol. Chem. 272:25190-25194(1997).
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORM 2).
RC   TISSUE=Tongue;
RX   MEDLINE=20175237; PubMed=10708588;
RA   Nagai M., Kyakumoto S., Sato N.;
RT   "Cancer cells responsible for humoral hypercalcemia express mRNA
RT   encoding a secreted form of ODF/TRANCE that induces osteoclast
RT   formation.";

RA   Galibert L.;
RT   "A homologue of the TNF receptor and its ligand enhance T-cell growth
RT   and dendritic-cell function.";
RL   Nature 390:175-179(1997).
RN   [5]
RP   SEQUENCE FROM N.A.
RA   Ikeda T.;
RL   Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: OSTEOCLAST DIFFERENTIATION AND ACTIVATION FACTOR.
CC   AUGMENTS ABILITY OF DENDRITIC CELLS TO STIMULATE NAIVE T-CELL
CC   PROLIFERATION. MAY BE AN IMPORTANT REGULATOR OF INTERACTIONS
CC   BETWEEN T CELLS AND DENDRITIC CELLS AND MAY PLAY A ROLE IN THE
CC   REGULATION OF THE T CELL-DEPENDENT IMMUNE RESPONSE.
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
CC   -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THYMUS AND LYMPH NODES BUT
CC   NOT IN B CELLS. A HIGH LEVEL EXPRESSION IS ALSO SEEN IN THE
CC   TRABECULAR BONE AND LUNG.
CC   -!- DISEASE: DEFICIENCY IN TNFSF11 RESULTS IN FAILURE TO FORM LOBULO-
CC   ALVEOLAR MAMMARY STRUCTURES DURING PREGNANCY, RESULTING IN DEATH
CC   OF NEWBORNS. TRANCE-DEFICIENT MICE SHOW SEVERE OSTEOPETROSIS, WITH
CC   NO OSTEOCLASTS, MARROW SPACES, OR TOOTH ERUPTION, AND EXHIBIT
CC   PROFOUND GROWTH RETARDATION AT SEVERAL SKELETAL SITES, INCLUDING
CC   THE LIMBS, SKULL, AND VERTEBRAE AND HAVE MARKED CHONDRODYSPLASIA,
CC   WITH THICK, IRREGULAR GROWTH PLATES AND A RELATIVE INCREASE IN
CC   HYPERTROPHIC CHONDROCYTES.
CC   -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC   ---
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---
DR   EMBL; AF053713; AAC40113.1; -.
DR   EMBL; AF013170; AAC71061.1; -.
DR   EMBL; AB008426; BAA25425.1; -.
DR   EMBL; AF019048; AAB86812.1; -.
DR   EMBL; AB036798; BAA97259.1; -.
DR   MGD; MGI:1100089; Tnfsf11.
DR   InterPro; IPR003363; TNF_5.
DR   InterPro; IPR000478; TNF_family.
DR   Pfam; PF00229; TNF; 1.
DR   ProDom; PD008600; TNF_5; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; FALSE_NEG.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Differentiation; Receptor; Glycoprotein; Transmembrane;
KW   Signal-anchor.
FT   DOMAIN   1   48   CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM   49   69   SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)
FT   (POTENTIAL).
FT   DOMAIN   70   316   EXTRACELLULAR (POTENTIAL).
FT   CARBOHYD   197   197   N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   262   262   N-LINKED (GLCNAC...) (POTENTIAL).
FT   CONFLICT   99   99   G -> D (IN REF. 4).
SQ   SEQUENCE   316 AA; 34944 MW; 08DF63A2BE00967A CRC64;

Query Match   100.0%; Score 1675; DB 1; Length 316;
Best Local Similarity   100.0%; Pred. No. 7.4e-13;
Matches 316; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MRRASRDYGKYLRSSEEMGSGPGVPHEGPLHPAPSAPAPPPAASRSMFLALLGLGLGQ 60
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MRRASRDYGKYLRSSEEMGSGPGVPHEGPLHPAPSAPAPPPAASRSMFLALLGLGLGQ 60

Qy 61 VVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESEDTLPDSCRRMKQ 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 61 VVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESEDTLPDSCRRMKQ 120
```

```
RL   Biochem. Biophys. Res. Commun. 269:532-536(2000).
CC   -!- FUNCTION: OSTEOCLAST DIFFERENTIATION AND ACTIVATION FACTOR.
CC       AUGMENTS ABILITY OF DENDRITIC CELLS TO STIMULATE NAIVE T-CELL
CC       PROLIFERATION. MAY BE AN IMPORTANT REGULATOR OF INTERACTIONS
CC       BETWEEN T CELLS AND DENDRITIC CELLS AND MAY PLAY A ROLE IN THE
CC       REGULATION OF THE T CELL-DEPENDENT IMMUNE RESPONSE. MAY ALSO PLAY
CC       AN IMPORTANT ROLE IN ENHANCED BONE-RESORPTION IN HUMORAL
CC       HYPERCALCEMIA OF MALIGNANCY.
CC   -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (ISOFORM 1) AND
CC       SECRETED (ISOFORM 2).
CC   -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2/SODF; ARE
CC       PRODUCED BY ALTERNATIVE SPLICING.
CC   -!- TISSUE SPECIFICITY: HIGHEST IN THE PERIPHERAL LYMPH NODES BUT
CC       WEAK IN SPLEEN, PERIPHERAL BLOOD LEUKOCYTES, BONE MARROW, HEART,
CC       PLACENTA, SKELETAL MUSCLE, STOMACH AND THYROID.
CC   -!- INDUCTION: UPREGULATED BY T CELL RECEPTOR STIMULATION.
CC   -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC   ----------------------------------------------------------------------
CC       This SWISS-PROT entry is copyright. It is produced through a collaboration
CC       between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC       the European Bioinformatics Institute. There are no restrictions on its
CC       use by non-profit institutions as long as its content is in no way
CC       modified and this statement is not removed. Usage by and for commercial
CC       entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC       or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AF019047; AAB86811.1; -.
DR   EMBL; AF053712; AAC39731.1; -.
DR   EMBL; AF013171; AAC51762.1; -.
DR   EMBL; AB037599; BAA90488.1; -.
DR   MIM; 602642; -.
DR   InterPro; IPR003263; TNF_5.
DR   InterPro; IPR000478; TNF_family.
DR   Pfam; PF00229; TNF; 1.
DR   ProDom; PD008600; TNF_5; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; FALSE_NEG.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Differentiation; Receptor; Glycoprotein; Transmembrane;
KW   Signal-anchor; Alternative splicing.
FT   DOMAIN        1     47       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     48     68       SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)
FT                                (POTENTIAL).
FT   DOMAIN       69    317       EXTRACELLULAR (POTENTIAL).
FT   CARBOHYD    171    171       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    198    198       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC      1     73       MISSING (IN ISOFORM 2).
FT   CONFLICT    194    194       A -> G (IN REF 3).
SEQUENCE   317 AA;  35478 MW;  76617644634809 7F CRC64;
```

Query Match   84.6%; Score 1417.5; DB 1; Length 317;
Best Local Similarity 84.3%; Pred. No. 1.2e-109;
Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;

```
Qy      1 MRRASRDYGKYLRSSEEMGSGPGVPHEGPLHPAPSAPAPPAASRSMFLALIGLGLGQ  60
          |||||||| ||||||||||| ||| |||||| || |||||||||||:||||||||||
Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLH-APPPAPHQPPAASRSMFVALLGLGLGQ  59

Qy     61 VVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESEDT--LPDSCRRM  118
          |||: ||||||||||||||||||||| |||||||||:|||||||||||||   :|||||||
Db     60 VVCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRI  119

Qy    119 KQAFQGAVQKELQHIVGPRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGS  178
          |||||||||||||||||| || :||||| ||:||||| | |||||||||| ||||
Db    120 KQAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGS  179

Qy    179 HKVTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLM  238
          ||:|||||||||||||||||||||||||||||||||||||||||||||| ::|:|||||
Db    180 HKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLM  239

Qy    239 VYYVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLL  298
          ||| |||||||| |||||||||| |||||||||||||||||||||||||| ||:||||||
Db    240 VYYVKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLL  299

Qy    299 DPDQDATYFGAFKVQDID  316
          |||||||||||||:|||
Db    300 DPDQDATYFGAFKVRDID  317
```

```
RESULT   3
TN10_HUMAN
ID   TN10_HUMAN     STANDARD;     PRT;    281 AA.
AC   P50591;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Tumor necrosis factor ligand superfamily member 10 (TNF-related
DE   apoptosis inducing ligand) (TRAIL protein) (Apo-2 ligand) (Apo-2L).
GN   TNFSF10 OR TRAIL OR APO2L.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96111955; PubMed=8777713;
RA   Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P.,
RA   Nicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A.,
RA   Goodwin R.G.;
RT   "Identification and characterization of a new member of the TNF
RT   family that induces apoptosis.";
RL   Immunity 3:673-682(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Placenta;
RX   MEDLINE=96278849; PubMed=8663110;
RA   Pitti R.M., Marsters S.A., Ruppert S., Donahue C.J., Moore A.,
RA   Ashkenazi A.;
RT   "Induction of apoptosis by Apo-2 ligand, a new member of the tumor
RT   necrosis factor cytokine family.";
RL   J. Biol. Chem. 271:12687-12690(1996).
RN   [3]
RP   X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 114-281.
RX   MEDLINE=20017054; PubMed=10549288;
RA   Hymowitz S.G., Christinger H.W., Fuh G., Ultsch M., O'Connell M.,
RA   Kelley R.F., Ashkenazi A., de Vos A.M.;
RT   "Triggering cell death: the crystal structure of Apo2L/TRAIL in a
RT   complex with death receptor 5.";
RL   Mol. Cell 4:563-571(1999).
RN   [4]
RP   X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 119-281.
RX   PubMed=10542098;
RA   Mongkolsapaya J., Grimes J.M., Chen N., Xu X.-N., Stuart D.I.,
RA   Jones E.Y., Screaton G.R.;
RT   "Structure of the TRAIL-DR5 complex reveals mechanisms conferring
RT   specificity in apoptotic initiation.";
RL   Nat. Struct. Biol. 6:1048-1053(1999).
CC   -!- FUNCTION: INDUCES APOPTOSIS.
CC   -!- SUBUNIT: HOMOTRIMER (POTENTIAL).
CC   -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (POTENTIAL).
CC   -!- TISSUE SPECIFICITY: WIDESPREAD; MOST PREDOMINANT IN SPLEEN, LUNG
CC       AND PROSTATE.
CC   -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC   ----------------------------------------------------------------------
CC       This SWISS-PROT entry is copyright. It is produced through a collaboration
CC       between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC       the European Bioinformatics Institute. There are no restrictions on its
CC       use by non-profit institutions as long as its content is in no way
CC       modified and this statement is not removed. Usage by and for commercial
CC       entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC       or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; U37518; AAC50332.1; -.
DR   EMBL; U57059; AAB01233.1; -.
DR   MIM; 603598; -.
```

```
DR   PDB; 1D0G; 22-OCT-99.
DR   PDB; 1D4V; 01-NOV-99.
DR   InterPro; IPR003263; TNF_5.
DR   InterPro; IPR003636; TNF_abc.
DR   InterPro; IPR000478; TNF_family.
DR   Pfam; PF00229; TNF; 1.
DR   ProDom; PD002012; TNF_abc; 1.
DR   ProDom; PD008600; TNF_5; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Transmembrane; Signal-anchor; Apoptosis; 3D-structure.
FT   DOMAIN      1     17      CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM   18     38      SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
FT   DOMAIN     39    281      EXTRACELLULAR (POTENTIAL).
SQ   SEQUENCE   281 AA;  32509 MW;  DDAAAF78DAAB2F6D CRC64;

Query Match             15.4%;  Score 258.5;  DB 1;  Length 281;
Best Local Similarity   26.4%;  Pred. No. 3.3e-14;
Matches   78;  Conservative   54;  Mismatches  113;  Indels  51;  Gaps  10;

Qy     43  PAASRSMFLALLGLGLGQVVCSIALFLYFRAQMD--PNRISEDSTHCFYRILRLHENAGL  100
Db     10  PSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACF-----LKEDDSY   64

Qy    101  QDSTLESEDTLPDSCRRMKQAFQGAVQK-----------ELQHIVGPQRFSGAPAMM  146
Db     65  WDP--NDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPL--------  113

Qy    147  EGSWLDVAQRGKPEAQPFAHLT-----INAASIPSGSHKVTL----SSWYHDR-GWAKIS  196
Db    114  ------VRERGPQRVA--AHTGTRGRSNTLSSPNSKNEKALGRKINSWESSRKSGHSFLS  165

Qy    197  NMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVYVVKTSIKIPSSHNLMK  256
Db    166  NLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKT-SYPDPILLMK  224

Qy    257  GGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKV  312
Db    225  SARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV  280

RESULT 4
TN10_MOUSE
ID   TN10_MOUSE     STANDARD;      PRT;   291 AA.
AC   P50592;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Tumor necrosis factor ligand superfamily member 10 (TNF-related
DE   apoptosis inducing ligand) (TRAIL protein).
GN   TNFSF10 OR TRAIL.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96111955; PubMed=8777713;
RA   Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P.,
RA   Nicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A.,
RA   Goodwin R.G.;
RT   "Identification and characterization of a new member of the TNF
RT   family that induces apoptosis.";
RL   Immunity 3:673-682(1995).
CC   -!- FUNCTION: INDUCES APOPTOSIS.
CC   -!- SUBUNIT: HOMOTRIMER (POTENTIAL).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
CC   -!- TISSUE SPECIFICITY: WIDESPREAD.
CC   -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC   --------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
DR   EMBL; U37522; AAC52345.1; -.
DR   MGD; MGI:107414; Tnfsf10.
DR   InterPro; IPR003263; TNF_5.
DR   InterPro; IPR003636; TNF_abc.
DR   InterPro; IPR000478; TNF_family.
DR   Pfam; PF00229; TNF; 1.
DR   ProDom; PD002012; TNF_abc; 1.
DR   ProDom; PD008600; TNF_5; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Transmembrane; Signal-anchor; Apoptosis.
FT   DOMAIN      1     17      CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM   18     38      SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
FT   DOMAIN     39    291      EXTRACELLULAR (POTENTIAL).
FT   CARBOHYD   52     52      N-LINKED (GLCNAC...) (POTENTIAL).
SQ   SEQUENCE   291 AA;  33477 MW;  3FEACAB9F0D7D802 CRC64;

Query Match             14.6%;  Score 244;  DB 1;  Length 291;
Best Local Similarity   27.5%;  Pred. No. 5.3e-13;
Matches   83;  Conservative   50;  Mismatches  111;  Indels  58;  Gaps  15;

Qy     52  ALLGLGLGQ------VVCSIAL---------------FLYFRAQMD--PNRISEDSTHCFYRIL   92
Db      6  ALKDLSFSQHFRMMVICIVLLQVLLQAVSVAVTYMYFTNEMKQLQDNYSKIGLACFSK-     63

Qy     93  RLHENAGLQDSTLESEDTLPDSC----RRMKQAFQGAVQKELQHIVG--PQRFSGAPAMM  146
Db     64  ---TDEDFWDST--DGEILNRPCLQVKRQLYQLIEEVTLRTFQDTISTVPEKQLSTPPLP  118

Qy    147  EGSWLDVAQRGKPEAQPFAHLT-----INAASIPSGSHKVTL---SSWYHDR-GWAKIS  196
Db    119  RG------GRPQ-KVAAHTGITRRSNSALIPISKDGKTLGQKIESWESSRKGHSFLN  169

Qy    197  NMTLSNGKLRVNQDGFYYLYANICFRHHE---TSGSVPTDYL--QLMVYVVKTSIKIPS  250
Db    170  HVLFRNGELVIEQEGLYIIYSQTYFRFQEAEDASKMVSKDKVRTKQLVQYIYKT-SYPD  228

Qy    251  SHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAF  310
Db    229  PIVLMKSARNSCWSRDAEYGLYSIYQGGLFELKKNDRIFVSVTNEHLMDLDQEASFFGAF  288

Qy    311  KV  312
Db    289  LI  290

RESULT 5
TNF5_BOVIN
ID   TNF5_BOVIN     STANDARD;      PRT;   261 AA.
AC   P51749;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   CD40 ligand (TNF-related activation protein) (TRAP) (T cell antigen
DE   GP39).
GN   TNFSF5 OR CD40LG OR CD40L.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Blood;
```